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Val	Arg	Ala	Trp	Ile	Glu	Lys	Thr	Leu	Glu	Glu	Gly	Arg	Lys	Arg	Gly
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Tyr	Val	Glu	Thr	Leu	Phe	Gly	Arg	Arg	Arg	Tyr	Val	Pro	Asp	Leu	Asn
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Ala	Arg	Val	Lys	Ser	Val	Arg	Glu	Ala	Ala	Glu	Arg	Met	Ala	Phe	Asn
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Met	Pro	Val	Gln	Gly	Thr	Ala	Ala	Asp	Leu	Met	Lys	Leu	Ala	Met	Val
		755					760					765			
Lys	Leu	Phe	Pro	Arg	Leu	Arg	Glu	Met	Gly	Ala	Arg	Met	Leu	Leu	Gln
	770					775					780				
Val	Ala	Asn	Glu	Leu	Leu	Leu	Glu	Ala	Pro	Gln	Ala	Arg	Ala	Glu	Glu
785					790					795					800
Val	Ala	Ala	Leu	Ala	Lys	Glu	Ala	Met	Glu	Lys	Ala	Tyr	Pro	Leu	Ala
				805					810					815	
Val	Pro	Leu	Glu	Val	Glu	Val	Gly	Met	Gly	Glu	Asp	Trp	Leu	Ser	Ala
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<210> 2815

<211> 881

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 2815

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Glu Tyr Phe Ser Gly Lys Lys Ile Ala Val Asp Ala Phe Asn Thr Leu
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Tyr Gln Phe Ile Ser Ile Ile Arg Gln Pro Asp Gly Thr Pro Leu Lys
 35 40 45

Asp Ser Gln Gly Arg Ile Thr Ser His Leu Ser Gly Ile Leu Tyr Arg
 50 55 60

Val Ser Asn Met Val Glu Val Gly Ile Arg Pro Val Phe Val Phe Asp
 65 70 75 80

Gly Glu Pro Pro Glu Phe Lys Lys Ala Glu Ile Glu Glu Arg Lys Lys

85

90

95

Arg Arg Ala Glu Ala Glu Glu Met Trp Ile Ala Ala Leu Gln Ala Gly
 100 105 110

Asp Lys Asp Ala Lys Lys Tyr Ala Gln Ala Ala Gly Arg Val Asp Glu
 115 120 125

Tyr Ile Val Asp Ser Ala Lys Thr Leu Leu Ser Tyr Met Gly Ile Pro
 130 135 140

Phe Val Asp Ala Pro Ser Glu Gly Glu Ala Gln Ala Ala Tyr Met Ala
 145 150 155 160

Ala Lys Gly Asp Val Glu Tyr Thr Gly Ser Gln Asp Tyr Asp Ser Leu
 165 170 175

Leu Phe Gly Ser Pro Arg Leu Ala Arg Asn Leu Ala Ile Thr Gly Lys
 180 185 190

Arg Lys Leu Pro Gly Lys Asn Val Tyr Val Asp Val Lys Pro Glu Ile
 195 200 205

Ile Ile Leu Glu Ser Asn Leu Lys Arg Leu Gly Leu Thr Arg Glu Gln
 210 215 220

Leu Ile Asp Ile Ala Ile Leu Val Gly Thr Asp Tyr Asn Glu Gly Val
 225 230 235 240

Lys Gly Val Gly Val Lys Lys Ala Leu Asn Tyr Ile Lys Thr Tyr Gly
 245 250 255

Asp Ile Phe Arg Ala Leu Lys Ala Leu Lys Val Asn Ile Asp His Val
 260 265 270

Glu Glu Ile Arg Asn Phe Phe Leu Asn Pro Pro Val Thr Asp Asp Tyr
 275 280 285

Arg Ile Glu Phe Arg Glu Pro Asp Phe Glu Lys Ala Ile Glu Phe Leu
 290 295 300

Cys Glu Glu His Asp Phe Ser Arg Glu Arg Val Glu Lys Ala Leu Glu
 305 310 315 320

Lys Leu Lys Ala Leu Lys Ser Thr Gln Ala Thr Leu Glu Arg Trp Phe
 325 330 335

Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu Gly Ala Phe Val Gly Phe
 340 345 350

Val Leu Ser Arg Pro Glu Pro Met Trp Ala Glu Leu Lys Ala Leu Ala
 355 360 365

Ala Cys Arg Gly Gly Arg Val His Arg Ala Ala Asp Pro Leu Ala Gly
 370 375 380

Leu Lys Asp Leu Lys Glu Val Arg Gly Leu Leu Ala Lys Asp Leu Ala
 385 390 395 400

Val Leu Ala Ser Arg Glu Gly Leu Asp Leu Val Pro Gly Asp Asp Pro
 405 410 415

Met Leu Leu Ala Tyr Leu Leu Gly Pro Ser Asn Thr Thr Pro Glu Gly
 420 425 430

Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu Asp Ala Ala His Arg
 435 440 445

Ala Leu Leu Ser Glu Arg Leu His Arg Asn Leu Leu Lys Arg Leu Glu
 450 455 460

Gly Glu Glu Lys Leu Leu Trp Leu Tyr His Glu Val Glu Lys Pro Leu
 465 470 475 480

Ser Arg Val Leu Ala His Met Glu Ala Thr Gly Val Arg Leu Asp Val
 485 490 495

Ala Tyr Leu Gln Ala Leu Ser Leu Glu Leu Ala Glu Glu Ile Arg Arg
 500 505 510

Leu Glu Glu Glu Val Phe Arg Leu Ala Gly His Pro Phe Asn Leu Asn
 515 520 525

Ser Arg Asp Gln Leu Glu Arg Val Leu Phe Asp Glu Leu Arg Leu Pro
 530 535 540

Ala Leu Lys Lys Thr Lys Lys Thr Gly Lys Arg Ser Thr Ser Ala Ala
 545 550 555 560

Val Leu Glu Ala Leu Arg Glu Ala His Pro Ile Val Glu Lys Ile Leu
 565 570 575

Gln His Arg Glu Leu Thr Lys Leu Lys Asn Thr Tyr Val Asp Pro Leu
 580 585 590

Pro Ser Leu Val His Pro Arg Thr Gly Arg Leu His Thr Arg Phe Asn
 595 600 605
 Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser Ser Asp Pro Asn Leu
 610 615 620
 Gln Asn Ile Pro Val Arg Thr Pro Leu Gly Gln Arg Ile Arg Arg Ala
 625 630 635 640
 Phe Val Ala Glu Ala Gly Trp Ala Leu Val Ala Leu Asp Tyr Ser Gln
 645 650 655
 Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly Asp Glu Asn Leu Ile
 660 665 670
 Arg Val Phe Gln Glu Gly Lys Asp Ile His Thr Gln Thr Ala Ser Trp
 675 680 685
 Met Phe Gly Val Pro Pro Glu Ala Val Asp Pro Leu Met Arg Arg Ala
 690 695 700
 Ala Lys Thr Val Asn Phe Gly Val Leu Tyr Gly Met Ser Ala His Arg
 705 710 715 720
 Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu Glu Ala Val Ala Phe Ile
 725 730 735
 Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val Arg Ala Trp Ile Glu Lys
 740 745 750
 Thr Leu Glu Glu Gly Arg Lys Arg Gly Tyr Val Glu Thr Leu Phe Gly
 755 760 765
 Arg Arg Arg Tyr Val Pro Asp Leu Asn Ala Arg Val Lys Ser Val Arg
 770 775 780
 Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro Val Gln Gly Thr Ala
 785 790 795 800
 Ala Asp Leu Met Lys Leu Ala Met Val Lys Leu Phe Pro Arg Leu Arg
 805 810 815
 Glu Met Gly Ala Arg Met Leu Leu Gln Val Ala Asn Glu Leu Leu Leu
 820 825 830
 Glu Ala Pro Gln Ala Arg Ala Glu Glu Val Ala Ala Leu Ala Lys Glu

835	840	845
Ala Met Glu Lys Ala Tyr Pro Leu Ala Val Pro Leu Glu Val Glu Val		
850	855	860
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His

<210> 2816

<211> 2619

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 2816

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<210> 2817

<211> 873

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 2817

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Glu Tyr Phe Ser Gly Lys Lys Ile Ala Val Asp Ala Phe Asn Thr Leu
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Tyr Gln Phe Ile Ser Ile Ile Arg Gln Pro Asp Gly Thr Pro Leu Lys
35 40 45

Asp Ser Gln Gly Arg Ile Thr Ser His Leu Ser Gly Ile Leu Tyr Arg
50 55 60

Val Ser Asn Met Val Glu Val Gly Ile Arg Pro Val Phe Val Phe Asp
65 70 75 80

Gly Glu Pro Pro Glu Phe Lys Lys Ala Glu Ile Glu Glu Arg Lys Lys
85 90 95

Arg Arg Ala Glu Ala Glu Glu Met Trp Ile Ala Ala Leu Gln Ala Gly
100 105 110

Asp Lys Asp Ala Lys Lys Tyr Ala Gln Ala Ala Gly Arg Val Asp Glu
115 120 125

Tyr Ile Val Asp Ser Ala Lys Thr Leu Leu Ser Tyr Met Gly Ile Pro
130 135 140

Phe Val Asp Ala Pro Ser Glu Gly Glu Ala Gln Ala Ala Tyr Met Ala
145 150 155 160

Ala Lys Gly Asp Val Glu Tyr Thr Gly Ser Gln Asp Tyr Asp Ser Leu
165 170 175

Leu Phe Gly Ser Pro Arg Leu Ala Arg Asn Leu Ala Ile Thr Gly Lys
180 185 190

Arg Lys Leu Pro Gly Lys Asn Val Tyr Val Asp Val Lys Pro Glu Ile
195 200 205

Ile Ile Leu Glu Ser Asn Leu Lys Arg Leu Gly Leu Thr Arg Glu Gln
 210 215 220

Leu Ile Asp Ile Ala Ile Leu Val Gly Thr Asp Tyr Asn Glu Gly Val
 225 230 235 240

Lys Gly Val Gly Val Lys Lys Ala Leu Asn Tyr Ile Lys Thr Tyr Gly
 245 250 255

Asp Ile Phe Arg Ala Leu Lys Ala Leu Lys Val Asn Ile Asp His Val
 260 265 270

Glu Glu Ile Arg Asn Phe Phe Leu Asn Pro Pro Val Thr Asp Asp Tyr
 275 280 285

Arg Ile Glu Phe Arg Glu Pro Asp Phe Glu Lys Ala Ile Glu Phe Leu
 290 295 300

Cys Glu Glu His Asp Phe Ser Arg Glu Arg Val Glu Lys Ala Leu Glu
 305 310 315 320

Lys Leu Lys Ala Leu Lys Ser Thr Leu Glu Glu Ala Pro Trp Pro Pro
 325 330 335

Pro Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro Met
 340 345 350

Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val His
 355 360 365

Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg
 370 375 380

Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu
 385 390 395 400

Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Gly
 405 410 415

Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu
 420 425 430

Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His
 435 440 445

Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu
 450 455 460

Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu
 465 470 475 480

Ala Thr Gly Val Arg Leu Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu
 485 490 495

Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu
 500 505 510

Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val
 515 520 525

Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys Thr
 530 535 540

Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala
 545 550 555 560

His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu
 565 570 575

Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr
 580 585 590

Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg
 595 600 605

Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro
 610 615 620

Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala
 625 630 635 640

Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His
 645 650 655

Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp
 660 665 670

Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala
 675 680 685

Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val
 690 695 700

Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro

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Lys	Val	Arg	Ala	Trp	Ile	Glu	Lys	Thr	Leu	Glu	Glu	Gly	Arg	Lys	Arg
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Asn	Met	Pro	Val	Gln	Gly	Thr	Ala	Ala	Asp	Leu	Met	Lys	Leu	Ala	Met
785					790					795					800
Val	Lys	Leu	Phe	Pro	Arg	Leu	Arg	Glu	Met	Gly	Ala	Arg	Met	Leu	Leu
				805					810					815	
Gln	Val	Ala	Asn	Glu	Leu	Leu	Leu	Glu	Ala	Pro	Gln	Ala	Arg	Ala	Glu
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Ala	Val	Pro	Leu	Glu	Val	Glu	Val	Gly	Met	Gly	Glu	Asp	Trp	Leu	Ser
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aacaccaccc	ccgagggggg	ggcgcggcgc	tacggggggg	agtggacgga	ggacgccgcc	1140
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gagaagctcc	tttggtctta	ccacgaggtg	gaaaagcccc	tctcccgggt	cctggcccat	1260
atggaggcca	ccgggggtacg	gctggacgtg	gcctaccttc	agggcctttc	cctggagctt	1320
gcggaggaga	tccgccgcct	cgaggaggag	gtcttccgct	tggcgggcca	ccccttcaac	1380
ctcaactccc	gggaccagct	ggaaaggggtg	ctctttgacg	agcttaggct	tccgccttg	1440
aagaagacga	agaagacagg	caagcgtccc	accagcgccg	cgggtgctgga	ggccctacgg	1500
gaggcccacc	ccatcgtgga	gaagatcctc	cagcaccggg	agctcaccaa	gctcaagaac	1560
acctacgtgg	acccccctcc	aagcctcgtc	cacccgagga	cgggcccgcct	ccacaccgc	1620
ttcaaccaga	cggccacggc	cacggggagg	cttagtagct	ccgaccccaa	cctgcagaac	1680
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agctggatgt	tcggcgctccc	cccggaggcc	gtggaccccc	tgatgcgccg	ggcggccaag	1920
acggtgaact	tcggcgctcct	ctacggcatg	tccgcccata	ggctctccca	ggagcttgcc	1980

atccccctacg aggaggcggt ggcctttata gagecgtact tccaaagctt cccaagggtg 2040
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<210> 2819

<211> 815

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 2819

Met Asn Ser Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu Val
 1 5 10 15

Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu Lys Gly Leu
 20 25 30

Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala Lys
 35 40 45

Ser Leu Leu Lys Ala Leu Arg Glu Asp Gly Asp Val Val Ile Val Val
 50 55 60

Phe Asp Ala Lys Ala Pro Ser Phe Arg His Gln Thr Tyr Glu Ala Tyr
 65 70 75 80

Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu Ala
 85 90 95

Leu Ile Lys Glu Met Val Asp Leu Leu Gly Leu Glu Arg Leu Glu Val
 100 105 110

Pro Gly Phe Glu Ala Asp Asp Val Leu Ala Thr Leu Ala Lys Lys Ala

115					120					125					
Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	Lys	Asp	Leu
130					135					140					
Tyr	Gln	Leu	Leu	Ser	Asp	Arg	Ile	His	Val	Leu	His	Pro	Glu	Gly	Tyr
145					150					155					160
Leu	Ile	Thr	Pro	Ala	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	Leu	Arg	Pro	Asp
				165					170					175	
Gln	Trp	Ala	Asp	Tyr	Arg	Ala	Leu	Thr	Gly	Asp	Glu	Ser	Asp	Asn	Leu
			180					185					190		
Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Arg	Lys	Leu	Leu	Glu
		195					200					205			
Glu	Trp	Gly	Ser	Leu	Glu	Ala	Leu	Leu	Lys	Asn	Leu	Asp	Arg	Leu	Lys
210					215					220					
Pro	Ala	Ile	Arg	Glu	Lys	Ile	Leu	Ala	His	Met	Asp	Asp	Leu	Lys	Leu
225					230					235					240
Ser	Trp	Asp	Leu	Ala	Lys	Val	Arg	Thr	Asp	Leu	Pro	Leu	Glu	Val	Asp
				245					250					255	
Phe	Ala	Lys	Arg	Arg	Glu	Pro	Asp	Arg	Glu	Gly	Glu	Lys	Pro	Arg	Glu
			260					265					270		
Glu	Ala	Pro	Trp	Pro	Pro	Pro	Glu	Gly	Ala	Phe	Val	Gly	Phe	Leu	Leu
		275					280					285			
Ser	Arg	Pro	Glu	Pro	Met	Trp	Ala	Glu	Leu	Lys	Ala	Leu	Ala	Ala	Cys
	290				295					300					
Arg	Gly	Gly	Arg	Val	His	Arg	Ala	Ala	Asp	Pro	Leu	Ala	Gly	Leu	Lys
305					310					315					320
Asp	Leu	Lys	Glu	Val	Arg	Gly	Leu	Leu	Ala	Lys	Asp	Leu	Ala	Val	Leu
				325					330					335	
Ala	Ser	Arg	Glu	Gly	Leu	Asp	Leu	Val	Pro	Gly	Asp	Asp	Pro	Met	Leu
			340					345					350		
Leu	Ala	Tyr	Leu	Leu	Gly	Pro	Ser	Asn	Thr	Thr	Pro	Glu	Gly	Val	Ala
		355					360					365			

Arg Arg Tyr Gly Gly Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu
 370 375 380

Leu Ser Glu Arg Leu His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu
 385 390 395 400

Glu Lys Leu Leu Trp Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg
 405 410 415

Val Leu Ala His Met Glu Ala Thr Gly Val Arg Leu Asp Val Ala Tyr
 420 425 430

Leu Gln Ala Leu Ser Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu
 435 440 445

Glu Glu Val Phe Arg Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg
 450 455 460

Asp Gln Leu Glu Arg Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu
 465 470 475 480

Lys Lys Thr Lys Lys Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu
 485 490 495

Glu Ala Leu Arg Glu Ala His Pro Ile Val Glu Lys Ile Leu Gln His
 500 505 510

Arg Glu Leu Thr Lys Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser
 515 520 525

Leu Val His Pro Arg Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr
 530 535 540

Ala Thr Ala Thr Gly Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn
 545 550 555 560

Ile Pro Val Arg Thr Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val
 565 570 575

Ala Glu Ala Gly Trp Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu
 580 585 590

Leu Arg Val Leu Ala His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val
 595 600 605

Phe Gln Glu Gly Lys Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe
 610 615 620

Gly Val Pro Pro Glu Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys
625 630 635 640

Thr Val Asn Phe Gly Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser
645 650 655

Gln Glu Leu Ala Ile Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg
660 665 670

Tyr Phe Gln Ser Phe Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu
675 680 685

Glu Glu Gly Arg Lys Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg
690 695 700

Arg Tyr Val Pro Asp Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala
705 710 715 720

Ala Glu Arg Met Ala Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp
725 730 735

Leu Met Lys Leu Ala Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met
740 745 750

Gly Ala Arg Met Leu Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala
755 760 765

Pro Gln Ala Arg Ala Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met
770 775 780

Glu Lys Ala Tyr Pro Leu Ala Val Pro Leu Glu Val Glu Val Gly Met
785 790 795 800

Gly Glu Asp Trp Leu Ser Ala Lys Gly His His His His His His
805 810 815

<210> 2820

<211> 2520

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 2820

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gaaccggtgc aggcggtcta cggcttcgcc aagagcctcc tcaaggccct caaggaggac	180
ggggacgcgg tgatcgtggt ctttgacgcc aaggccccct ccttcgccca cgaggcctac	240
ggggggtaca aggcggggccg ggccccacc cgggaggact tccccgccca gctcgccttg	300
gtcaagcggc tgggtggacct tctgggcctg gtccgcctcg agggcccggt gtacgaggcg	360
gacgacgtcc tgggcaccct ggccaagaag gccgaaaagg aggggtacga ggtgcgcac	420
ctcaccgcgg accgcgacct ctaccaactc gtctccgacc gcatccacgt cctccacccc	480
gaggggtacc tcatcacccc ggagtggctt tgggagaagt atgggcttaa gccttcccag	540
tgggtggact accgggcctt ggccggggac ccttcgcaca acatccccgg cgtgaagggc	600
atcggggaga agacggcggc caagctgac cgggagtggt gaagcctgga aaacctcctc	660
aagaacctgg accggctgaa gcccgccatc cgggagaaga tcctggccca catggacgat	720
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```

ctcgcccacc tctccgggga cgaaaacctg atcaggggtct tccaggaggg gaaggacatc 1920
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<210> 2821

<211> 840

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 2821

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Leu Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu
          20          25          30

```

```

Lys Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly
          35          40          45

```

```

Phe Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val
          50          55          60

```

```

Ile Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr
65          70          75          80

```

```

Gly Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg
          85          90          95

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Gln Leu Ala Leu Val Lys Arg Leu Val Asp Leu Leu Gly Leu Val Arg
 100 105 110

Leu Glu Ala Pro Gly Tyr Glu Ala Asp Asp Val Leu Gly Thr Leu Ala
 115 120 125

Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp
 130 135 140

Arg Asp Leu Tyr Gln Leu Val Ser Asp Arg Ile His Val Leu His Pro
 145 150 155 160

Glu Gly Tyr Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly Leu
 165 170 175

Lys Pro Ser Gln Trp Val Asp Tyr Arg Ala Leu Ala Gly Asp Pro Ser
 180 185 190

Asp Asn Ile Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Ala Lys
 195 200 205

Leu Ile Arg Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu Asp
 210 215 220

Arg Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp
 225 230 235 240

Leu Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu
 245 250 255

Glu Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg
 260 265 270

Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly
 275 280 285

Leu Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro
 290 295 300

Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro Met Trp
 305 310 315 320

Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val His Arg
 325 330 335

Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly
 340 345 350

Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp
355 360 365

Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Gly Pro
370 375 380

Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp
385 390 395 400

Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg
405 410 415

Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr
420 425 430

His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala
435 440 445

Thr Gly Val Arg Leu Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu
450 455 460

Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala
465 470 475 480

Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu
485 490 495

Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys Thr Gly
500 505 510

Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His
515 520 525

Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys
530 535 540

Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly
545 550 555 560

Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu
565 570 575

Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu
580 585 590

Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu

595					600					605					
Val	Ala	Leu	Asp	Tyr	Ser	Gln	Ile	Glu	Leu	Arg	Val	Leu	Ala	His	Leu
610						615					620				
Ser	Gly	Asp	Glu	Asn	Leu	Ile	Arg	Val	Phe	Gln	Glu	Gly	Lys	Asp	Ile
625					630					635					640
His	Thr	Gln	Thr	Ala	Ser	Trp	Met	Phe	Gly	Val	Pro	Pro	Glu	Ala	Val
				645					650					655	
Asp	Pro	Leu	Met	Arg	Arg	Ala	Ala	Lys	Thr	Val	Asn	Phe	Gly	Val	Leu
			660					665					670		
Tyr	Gly	Met	Ser	Ala	His	Arg	Leu	Ser	Gln	Glu	Leu	Ala	Ile	Pro	Tyr
		675					680					685			
Glu	Glu	Ala	Val	Ala	Phe	Ile	Glu	Arg	Tyr	Phe	Gln	Ser	Phe	Pro	Lys
	690					695					700				
Val	Arg	Ala	Trp	Ile	Glu	Lys	Thr	Leu	Glu	Glu	Gly	Arg	Lys	Arg	Gly
705					710					715					720
Tyr	Val	Glu	Thr	Leu	Phe	Gly	Arg	Arg	Arg	Tyr	Val	Pro	Asp	Leu	Asn
				725					730					735	
Ala	Arg	Val	Lys	Ser	Val	Arg	Glu	Ala	Ala	Glu	Arg	Met	Ala	Phe	Asn
			740					745					750		
Met	Pro	Val	Gln	Gly	Thr	Ala	Ala	Asp	Leu	Met	Lys	Leu	Ala	Met	Val
		755				760						765			
Lys	Leu	Phe	Pro	Arg	Leu	Arg	Glu	Met	Gly	Ala	Arg	Met	Leu	Leu	Gln
	770					775					780				
Val	Ala	Asn	Glu	Leu	Leu	Leu	Glu	Ala	Pro	Gln	Ala	Arg	Ala	Glu	Glu
785					790					795					800
Val	Ala	Ala	Leu	Ala	Lys	Glu	Ala	Met	Glu	Lys	Ala	Tyr	Pro	Leu	Ala
				805					810					815	
Val	Pro	Leu	Glu	Val	Glu	Val	Gly	Met	Gly	Glu	Asp	Trp	Leu	Ser	Ala
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Lys	Gly	His	His	His	His	His	His	His							
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<210> 2822

<211> 2445

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 2822

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caggcgggtg acgggtttgc caagagcctt ttgaaggcgc taagggaaga cggggatgtg     180
gtgatcgtgg tgtttgacgc caaggccccc tccttccgcc accagacctt cgaggcctac     240
aaggcggggc gggctccac ccccgaggac tttccccggc agcttgcctt tatcaaggag     300
atggtggacc ttttgggctt taccgcctc gaggtgccgg gctttgaagc ggatgacgtc     360
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<210> 2823

<211> 815

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 2823

Met Asn Ser Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu Val
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Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu Lys Gly Leu
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Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala Lys
35 40 45

Ser Leu Leu Lys Ala Leu Arg Glu Asp Gly Asp Val Val Ile Val Val
 50 55 60

Phe Asp Ala Lys Ala Pro Ser Phe Arg His Gln Thr Tyr Glu Ala Tyr
 65 70 75 80

Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu Ala
 85 90 95

Leu Ile Lys Glu Met Val Asp Leu Leu Gly Phe Thr Arg Leu Glu Val
 100 105 110

Pro Gly Phe Glu Ala Asp Asp Val Leu Ala Thr Leu Ala Lys Lys Ala
 115 120 125

Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys Asp Leu
 130 135 140

Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu Gly Tyr
 145 150 155 160

Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg Pro Asp
 165 170 175

Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp Asn Leu
 180 185 190

Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu Leu Glu
 195 200 205

Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg Leu Lys
 210 215 220

Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu Lys Leu
 225 230 235 240

Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu Val Asp
 245 250 255

Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Gly Glu Lys Pro Arg Glu
 260 265 270

Glu Ala Pro Trp Pro Pro Pro Glu Gly Ala Phe Val Gly Phe Leu Leu
 275 280 285

Ser Arg Pro Glu Pro Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys
 290 295 300

Arg Gly Gly Arg Val His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys
 305 310 315 320
 Asp Leu Lys Glu Val Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu
 325 330 335
 Ala Ser Arg Glu Gly Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu
 340 345 350
 Leu Ala Tyr Leu Leu Gly Pro Ser Asn Thr Thr Pro Glu Gly Val Ala
 355 360 365
 Arg Arg Tyr Gly Gly Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu
 370 375 380
 Leu Ser Glu Arg Leu His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu
 385 390 395 400
 Glu Lys Leu Leu Trp Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg
 405 410 415
 Val Leu Ala His Met Glu Ala Thr Gly Val Arg Leu Asp Val Ala Tyr
 420 425 430
 Leu Gln Ala Leu Ser Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu
 435 440 445
 Glu Glu Val Phe Arg Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg
 450 455 460
 Asp Gln Leu Glu Arg Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu
 465 470 475 480
 Lys Lys Thr Lys Lys Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu
 485 490 495
 Glu Ala Leu Arg Glu Ala His Pro Ile Val Glu Lys Ile Leu Gln His
 500 505 510
 Arg Glu Leu Thr Lys Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser
 515 520 525
 Leu Val His Pro Arg Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr
 530 535 540
 Ala Thr Ala Thr Gly Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn

545		550		555		560									
Ile	Pro	Val	Arg	Thr	Pro	Leu	Gly	Gln	Arg	Ile	Arg	Arg	Ala	Phe	Val
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Ala	Glu	Ala	Gly	Trp	Ala	Leu	Val	Ala	Leu	Asp	Tyr	Ser	Gln	Ile	Glu
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Leu	Arg	Val	Leu	Ala	His	Leu	Ser	Gly	Asp	Glu	Asn	Leu	Ile	Arg	Val
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Phe	Gln	Glu	Gly	Lys	Asp	Ile	His	Thr	Gln	Thr	Ala	Ser	Trp	Met	Phe
	610					615					620				
Gly	Val	Pro	Pro	Glu	Ala	Val	Asp	Pro	Leu	Met	Arg	Arg	Ala	Ala	Lys
625					630					635					640
Thr	Val	Asn	Phe	Gly	Val	Leu	Tyr	Gly	Met	Ser	Ala	His	Arg	Leu	Ser
				645					650					655	
Gln	Glu	Leu	Ala	Ile	Pro	Tyr	Glu	Glu	Ala	Val	Ala	Phe	Ile	Glu	Arg
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Tyr	Phe	Gln	Ser	Phe	Pro	Lys	Val	Arg	Ala	Trp	Ile	Glu	Lys	Thr	Leu
		675					680					685			
Glu	Glu	Gly	Arg	Lys	Arg	Gly	Tyr	Val	Glu	Thr	Leu	Phe	Gly	Arg	Arg
	690					695					700				
Arg	Tyr	Val	Pro	Asp	Leu	Asn	Ala	Arg	Val	Lys	Ser	Val	Arg	Glu	Ala
705					710					715					720
Ala	Glu	Arg	Met	Ala	Phe	Asn	Met	Pro	Val	Gln	Gly	Thr	Ala	Ala	Asp
				725					730					735	
Leu	Met	Lys	Leu	Ala	Met	Val	Lys	Leu	Phe	Pro	Arg	Leu	Arg	Glu	Met
			740					745					750		
Gly	Ala	Arg	Met	Leu	Leu	Gln	Val	Ala	Asn	Glu	Leu	Leu	Leu	Glu	Ala
		755					760					765			
Pro	Gln	Ala	Arg	Ala	Glu	Glu	Val	Ala	Ala	Leu	Ala	Lys	Glu	Ala	Met
	770					775					780				
Glu	Lys	Ala	Tyr	Pro	Leu	Ala	Val	Pro	Leu	Glu	Val	Glu	Val	Gly	Met
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Gly Glu Asp Trp Leu Ser Ala Lys Gly His His His His His His
805 810 815

<210> 2824

<211> 2520

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 2824

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gaaccggtgc aggcggtcta cggcttcgcc aagagcctcc tcaaggccct caaggaggac	180
ggggacgcgg tgatcgtggt ctttgacgcc aaggccccct ccttccgcca cgaggcctac	240
ggggggtaca aggcggggccg ggccccacc ccggaggact tccccgcca gctcgccttg	300
gtcaagcggc tgggtggacct tctgggcttt accgcctcg agggcccggg gtacgaggcg	360
gacgacgtcc tgggcaccct ggccaagaag gccgaaaagg aggggtacga ggtgcgcac	420
ctcaccgcgg accgcgacct ctaccaactc gtctccgacc gcatccacgt cctccacccc	480
gaggggtacc tcatcacccc ggagtggctt tgggagaagt atgggcttaa gccttcccag	540
tgggtggact accgggcctt ggccggggac ccttccgaca acatccccgg cgtgaagggc	600
atcggggaga agacggcggc caagctgac cgaggagtgg gaagcctgga aaacctctc	660
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<210> 2825

<211> 840

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 2825

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Leu Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu

- 2030 -

Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly
 275 280 285

Leu Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro
 290 295 300

Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro Met Trp
 305 310 315 320

Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val His Arg
 325 330 335

Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly
 340 345 350

Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp
 355 360 365

Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Gly Pro
 370 375 380

Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp
 385 390 395 400

Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg
 405 410 415

Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr
 420 425 430

His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala
 435 440 445

Thr Gly Val Arg Leu Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu
 450 455 460

Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala
 465 470 475 480

Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu
 485 490 495

Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys Thr Gly
 500 505 510

Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His
 515 520 525

Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys
530 535 540

Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly
545 550 555 560

Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu
565 570 575

Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu
580 585 590

Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu
595 600 605

Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu
610 615 620

Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp Ile
625 630 635 640

His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val
645 650 655

Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu
660 665 670

Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr
675 680 685

Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys
690 695 700

Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly
705 710 715 720

Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn
725 730 735

Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn
740 745 750

Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val
755 760 765

Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln

770

775

780

Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu
785 790 795 800

Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu Ala
805 810 815

Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu Ser Ala
820 825 830

Lys Gly His His His His His His
835 840

<210> 2826

<211> 2445

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 2826

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tcctgggacc tggccaaggt gcgcaccgac ctgcccctgg aggtggactt cgccaaaagg    780
cgggagcccg accgggaggg ggagaagccc cgggaggagg cccctggcc cccgcccga      840

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<210> 2827

<211> 815

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 2827

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20 25 30

Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala Lys
35 40 45

Ser Leu Leu Lys Ala Leu Arg Glu Asp Gly Asp Val Val Ile Val Val
50 55 60

Phe Asp Ala Glu Ala Pro Ser Phe Arg His Gln Thr Tyr Glu Ala Tyr
65 70 75 80

Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu Ala
85 90 95

Leu Ile Lys Glu Met Val Asp Leu Leu Gly Leu Glu Arg Leu Glu Val
100 105 110

Pro Gly Phe Glu Ala Asp Asp Val Leu Ala Thr Leu Ala Lys Lys Ala
115 120 125

Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys Asp Leu
130 135 140

Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu Gly Tyr
145 150 155 160

Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg Pro Asp
165 170 175

Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp Asn Leu
180 185 190

Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu Leu Glu
195 200 205

Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg Leu Lys
210 215 220

Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu Lys Leu
 225 230 235 240
 Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu Val Asp
 245 250 255
 Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Gly Glu Lys Pro Arg Glu
 260 265 270
 Glu Ala Pro Trp Pro Pro Pro Glu Gly Ala Phe Val Gly Phe Leu Leu
 275 280 285
 Ser Arg Pro Glu Pro Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys
 290 295 300
 Arg Gly Gly Arg Val His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys
 305 310 315 320
 Asp Leu Lys Glu Val Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu
 325 330 335
 Ala Ser Arg Glu Gly Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu
 340 345 350
 Leu Ala Tyr Leu Leu Gly Pro Ser Asn Thr Thr Pro Glu Gly Val Ala
 355 360 365
 Arg Arg Tyr Gly Gly Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu
 370 375 380
 Leu Ser Glu Arg Leu His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu
 385 390 395 400
 Glu Lys Leu Leu Trp Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg
 405 410 415
 Val Leu Ala His Met Glu Ala Thr Gly Val Arg Leu Asp Val Ala Tyr
 420 425 430
 Leu Gln Ala Leu Ser Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu
 435 440 445
 Glu Glu Val Phe Arg Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg
 450 455 460
 Asp Gln Leu Glu Arg Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu

465					470						475				480
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Ile	Pro	Val	Arg	Thr	Pro	Leu	Gly	Gln	Arg	Ile	Arg	Arg	Ala	Phe	Val
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Phe	Gln	Glu	Gly	Lys	Asp	Ile	His	Thr	Gln	Thr	Ala	Ser	Trp	Met	Phe
	610					615					620				
Gly	Val	Pro	Pro	Glu	Ala	Val	Asp	Pro	Leu	Met	Arg	Arg	Ala	Ala	Lys
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Thr	Val	Asn	Phe	Gly	Val	Leu	Tyr	Gly	Met	Ser	Ala	His	Arg	Leu	Ser
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Gln	Glu	Leu	Ala	Ile	Pro	Tyr	Glu	Glu	Ala	Val	Ala	Phe	Ile	Glu	Arg
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Tyr	Phe	Gln	Ser	Phe	Pro	Lys	Val	Arg	Ala	Trp	Ile	Glu	Lys	Thr	Leu
		675					680					685			
Glu	Glu	Gly	Arg	Lys	Arg	Gly	Tyr	Val	Glu	Thr	Leu	Phe	Gly	Arg	Arg
	690					695					700				
Arg	Tyr	Val	Pro	Asp	Leu	Asn	Ala	Arg	Val	Lys	Ser	Val	Arg	Glu	Ala
705					710					715					720

Ala Glu Arg Met Ala Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp
725 730 735

Leu Met Lys Leu Ala Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met
740 745 750

Gly Ala Arg Met Leu Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala
755 760 765

Pro Gln Ala Arg Ala Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met
770 775 780

Glu Lys Ala Tyr Pro Leu Ala Val Pro Leu Glu Val Glu Val Gly Met
785 790 795 800

Gly Glu Asp Trp Leu Ser Ala Lys Gly His His His His His His
805 810 815

<210> 2828

<211> 2445

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 2828

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<210> 2829

<211> 815

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 2829

Met Asn Ser Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu Val
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Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu Lys Gly Leu
20 25 30

Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala Lys
35 40 45

Ser Leu Leu Lys Ala Leu Arg Glu Asp Gly Asp Val Val Ile Val Val
50 55 60

Phe Asp Ala Glu Ala Pro Ser Phe Arg His Gln Thr Tyr Glu Ala Tyr
65 70 75 80

Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu Ala
85 90 95

Leu Ile Lys Glu Met Val Asp Leu Leu Gly Phe Thr Arg Leu Glu Val
100 105 110

Pro Gly Phe Glu Ala Asp Asp Val Leu Ala Thr Leu Ala Lys Lys Ala
115 120 125

Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys Asp Leu
130 135 140

Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu Gly Tyr
145 150 155 160

Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg Pro Asp
165 170 175

Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp Asn Leu
180 185 190

Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu Leu Glu
195 200 205

Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg Leu Lys
 210 215 220

Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu Lys Leu
 225 230 235 240

Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu Val Asp
 245 250 255

Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Gly Glu Lys Pro Arg Glu
 260 265 270

Glu Ala Pro Trp Pro Pro Pro Glu Gly Ala Phe Val Gly Phe Leu Leu
 275 280 285

Ser Arg Pro Glu Pro Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys
 290 295 300

Arg Gly Gly Arg Val His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys
 305 310 315 320

Asp Leu Lys Glu Val Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu
 325 330 335

Ala Ser Arg Glu Gly Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu
 340 345 350

Leu Ala Tyr Leu Leu Gly Pro Ser Asn Thr Thr Pro Glu Gly Val Ala
 355 360 365

Arg Arg Tyr Gly Gly Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu
 370 375 380

Leu Ser Glu Arg Leu His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu
 385 390 395 400

Glu Lys Leu Leu Trp Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg
 405 410 415

Val Leu Ala His Met Glu Ala Thr Gly Val Arg Leu Asp Val Ala Tyr
 420 425 430

Leu Gln Ala Leu Ser Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu
 435 440 445

Glu Glu Val Phe Arg Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg

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Asp Gln Leu Glu Arg Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu				
465		470		475 480
Lys Lys Thr Lys Lys Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu				
	485		490	495
Glu Ala Leu Arg Glu Ala His Pro Ile Val Glu Lys Ile Leu Gln His				
	500		505	510
Arg Glu Leu Thr Lys Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser				
	515		520	525
Leu Val His Pro Arg Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr				
	530		535	540
Ala Thr Ala Thr Gly Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn				
	545		550	555 560
Ile Pro Val Arg Thr Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val				
	565		570	575
Ala Glu Ala Gly Trp Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu				
	580		585	590
Leu Arg Val Leu Ala His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val				
	595		600	605
Phe Gln Glu Gly Lys Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe				
	610		615	620
Gly Val Pro Pro Glu Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys				
	625		630	635 640
Thr Val Asn Phe Gly Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser				
	645		650	655
Gln Glu Leu Ala Ile Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg				
	660		665	670
Tyr Phe Gln Ser Phe Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu				
	675		680	685
Glu Glu Gly Arg Lys Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg				
	690		695	700

Arg Tyr Val Pro Asp Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala
705 710 715 720

Ala Glu Arg Met Ala Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp
725 730 735

Leu Met Lys Leu Ala Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met
740 745 750

Gly Ala Arg Met Leu Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala
755 760 765

Pro Gln Ala Arg Ala Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met
770 775 780

Glu Lys Ala Tyr Pro Leu Ala Val Pro Leu Glu Val Glu Val Gly Met
785 790 795 800

Gly Glu Asp Trp Leu Ser Ala Lys Gly His His His His His His
805 810 815

<210> 2830

<211> 2520

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 2830

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gagccggtcc aggcggtgta cgggtttgcc aagagccttt tgaaggcgct aagagaagac      180
ggggacgcgg tgatcgtggt ctttgacgcc gagggcccct ccttccgcca cgaggcctac      240
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gaggggtacc tcatcacccc ggctggctt tgggaaaagt acggcctgag gcccgaccag      540
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<211> 840

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 2831

Met Asn Ser Glu Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val
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Leu Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu
20 25 30

Lys Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly
35 40 45

Phe Ala Lys Ser Leu Leu Lys Ala Leu Arg Glu Asp Gly Asp Ala Val
50 55 60

Ile Val Val Phe Asp Ala Glu Ala Pro Ser Phe Arg His Glu Ala Tyr
65 70 75 80

Gly Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg
85 90 95

Gln Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr Arg
100 105 110

Leu Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu Ala
115 120 125

Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp
130 135 140

Lys Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro
145 150 155 160

Glu Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu
165 170 175

Arg Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser
180 185 190

Asp Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu Lys
195 200 205

Leu Leu Lys Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp
210 215 220

Arg Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp
225 230 235 240

Leu Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu
245 250 255

Glu Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Gly Leu Lys
260 265 270

Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly
275 280 285

Leu Leu Gly Gly Glu Lys Pro Arg Glu Glu Ala Pro Trp Pro Pro Pro
290 295 300

Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp
305 310 315 320

Ala Asp Leu Leu Ala Leu Ala Ala Cys Arg Gly Gly Arg Val His Arg
325 330 335

Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly
340 345 350

Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp
355 360 365

Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Gly Pro
370 375 380

Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp
385 390 395 400

Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg
405 410 415

Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr
420 425 430

His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala
435 440 445

Thr Gly Val Arg Leu Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu
450 455 460

Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala
465 470 475 480

Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu
485 490 495

Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys Thr Gly
500 505 510

Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His
515 520 525

Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys
530 535 540

Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly
545 550 555 560

Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu
565 570 575

Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu
580 585 590

Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu
595 600 605

Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu
610 615 620

Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp Ile
625 630 635 640

His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val
645 650 655

Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu
660 665 670

Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr

675					680					685					
Glu	Glu	Ala	Val	Ala	Phe	Ile	Glu	Arg	Tyr	Phe	Gln	Ser	Phe	Pro	Lys
690						695					700				
Val	Arg	Ala	Trp	Ile	Glu	Lys	Thr	Leu	Glu	Glu	Gly	Arg	Lys	Arg	Gly
705					710					715					720
Tyr	Val	Glu	Thr	Leu	Phe	Gly	Arg	Arg	Arg	Tyr	Val	Pro	Asp	Leu	Asn
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Ala	Arg	Val	Lys	Ser	Val	Arg	Glu	Ala	Ala	Glu	Arg	Met	Ala	Phe	Asn
			740					745					750		
Met	Pro	Val	Gln	Gly	Thr	Ala	Ala	Asp	Leu	Met	Lys	Leu	Ala	Met	Val
		755					760					765			
Lys	Leu	Phe	Pro	Arg	Leu	Arg	Glu	Met	Gly	Ala	Arg	Met	Leu	Leu	Gln
	770					775					780				
Val	Ala	Asn	Glu	Leu	Leu	Leu	Glu	Ala	Pro	Gln	Ala	Arg	Ala	Glu	Glu
785					790					795					800
Val	Ala	Ala	Leu	Ala	Lys	Glu	Ala	Met	Glu	Lys	Ala	Tyr	Pro	Leu	Ala
				805					810					815	
Val	Pro	Leu	Glu	Val	Glu	Val	Gly	Met	Gly	Glu	Asp	Trp	Leu	Ser	Ala
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<210> 2833

<211> 842

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 2833

Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu
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Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu Lys
 20 25 30

Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Met Val Tyr Gly Phe
 35 40 45

Ala Arg Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Gln Ala Val Val
 50 55 60

Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Glu
 65 70 75 80

Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln
 85 90 95

Leu Ala Leu Ile Lys Glu Met Val Asp Leu Leu Gly Leu Ala Arg Leu

100	105	110
Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu Ala Lys		
115	120	125
Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Arg		
130	135	140
Asp Leu Tyr Gln Leu Val Ser Asp Arg Val Ala Val Leu His Pro Glu		
145	150	155
Gly His Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly Leu Arg		
165	170	175
Pro Glu Gln Trp Val Asp Phe Arg Ala Leu Val Gly Asp Pro Ser Asp		
180	185	190
Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Ala Lys Leu		
195	200	205
Ile Arg Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys His Leu Glu Gln		
210	215	220
Val Lys Pro Ala Ser Val Arg Glu Lys Ile Leu Ser His Met Glu Asp		
225	230	235
Leu Lys Leu Ser Leu Glu Leu Ser Arg Val His Thr Asp Leu Leu Leu		
245	250	255
Gln Val Asp Phe Lys Ala Leu Arg Arg Arg Thr Pro Asp Leu Glu Gly		
260	265	270
Leu Arg Ala Phe Leu Glu Glu Leu Glu Phe Gly Ser Leu Leu His Glu		
275	280	285
Phe Gly Leu Leu Glu Ala Pro Ala Ala Ala Glu Glu Ala Pro Trp Pro		
290	295	300
Pro Pro Glu Gly Ala Phe Val Gly Tyr Val Leu Ser Arg Pro Glu Pro		
305	310	315
Met Trp Ala Glu Leu Asn Ala Leu Ala Ala Ala Trp Gly Gly Arg Val		
325	330	335
His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val		
340	345	350

Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly
 355 360 365

Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu
 370 375 380

Gly Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly
 385 390 395 400

Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu
 405 410 415

His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp
 420 425 430

Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met
 435 440 445

Glu Ala Thr Gly Val Arg Leu Asp Val Ala Tyr Leu Gln Ala Leu Ser
 450 455 460

Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg
 465 470 475 480

Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg
 485 490 495

Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys
 500 505 510

Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu
 515 520 525

Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys
 530 535 540

Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg
 545 550 555 560

Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly
 565 570 575

Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr
 580 585 590

Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp
 595 600 605

Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala
610 615 620

His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys
625 630 635 640

Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu
645 650 655

Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly
660 665 670

Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile
675 680 685

Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe
690 695 700

Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys
705 710 715 720

Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp
725 730 735

Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala
740 745 750

Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala
755 760 765

Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu
770 775 780

Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala
785 790 795 800

Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro
805 810 815

Leu Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu
820 825 830

Ser Ala Lys Gly His His His His His His
835 840

<210> 2834

<211> 2511

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 2834

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caggcgggtgt acgggtttgc caagagcctt ttgaaggcgc taagagaaga cggggatgtg      180
gtgatcgtgg tctttgacgc caaggccccc tcttccgcc acgaggccta cggggggtac      240
aaggcggggc gggcccccgc ccccgaggac ttcccccggc agctcgccct catcaaggag      300
ctggtggacc tcctggggct ggcgcgcctc gaggtgccgg gctttgaagc ggatgacgtc      360
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cccgagggag ccttcgtggg gtacgttctt tcccgccccg agcccatgtg ggcggagctt      960
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gggatggggg aggactggct ttccgccaag ggtcaccacc accaccacca c 2511

<210> 2835

<211> 837

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 2835

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Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys Gly Leu
20 25 30

Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala Lys
35 40 45

Ser Leu Leu Lys Ala Leu Arg Glu Asp Gly Asp Val Val Ile Val Val
 50 55 60

Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly Gly Tyr
 65 70 75 80

Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu Ala
 85 90 95

Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu Glu Val
 100 105 110

Pro Gly Phe Glu Ala Asp Asp Val Leu Ala Thr Leu Ala Lys Lys Ala
 115 120 125

Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Gly Asp Arg Asp Leu
 130 135 140

Tyr Gln Leu Val Ser Asp Arg Val Ala Val Leu His Pro Glu Gly His
 145 150 155 160

Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly Leu Arg Pro Glu
 165 170 175

Gln Trp Val Asp Tyr Arg Ala Leu Ala Gly Asp Pro Ser Asp Asn Ile
 180 185 190

Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu Leu Glu
 195 200 205

Glu Trp Gly Ser Val Glu Ala Leu Leu Lys Asn Leu Asp Arg Leu Lys
 210 215 220

Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Glu Asp Leu Lys Leu
 225 230 235 240

Ser Leu Glu Leu Ser Arg Val Arg Thr Asp Leu Pro Leu Glu Val Asp
 245 250 255

Leu Ala Gln Gly Arg Glu Pro Asp Arg Glu Gly Leu Lys Ala Phe Leu
 260 265 270

Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu Leu Glu
 275 280 285

Ser Pro Val Ala Ala Glu Glu Ala Pro Trp Pro Pro Pro Glu Gly Ala
 290 295 300

Phe Val Gly Tyr Val Leu Ser Arg Pro Glu Pro Met Trp Ala Glu Leu
 305 310 315 320

Asn Ala Leu Ala Ala Ala Trp Gly Gly Arg Val His Arg Ala Ala Asp
 325 330 335

Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly Leu Leu Ala
 340 345 350

Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp Leu Val Pro
 355 360 365

Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Gly Pro Ser Asn Thr
 370 375 380

Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu Asp
 385 390 395 400

Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg Asn Leu Leu
 405 410 415

Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr His Glu Val
 420 425 430

Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr Gly Val
 435 440 445

Arg Leu Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu Leu Ala Glu
 450 455 460

Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala Gly His Pro
 465 470 475 480

Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe Asp Glu
 485 490 495

Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys Thr Gly Lys Arg Ser
 500 505 510

Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro Ile Val
 515 520 525

Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys Asn Thr Tyr
 530 535 540

Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly Arg Leu His

545		550		555		560
Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser Ser						
		565		570		575
Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly Gln Arg						
		580		585		590
Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu Val Ala Leu						
		595		600		605
Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly Asp						
		610		615		620
Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp Ile His Thr Gln						
		625		630		640
Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val Asp Pro Leu						
		645		650		655
Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu Tyr Gly Met						
		660		665		670
Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu Glu Ala						
		675		680		685
Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val Arg Ala						
		690		695		700
Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly Tyr Val Glu						
		705		710		720
Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn Ala Arg Val						
		725		730		735
Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro Val						
		740		745		750
Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys Leu Phe						
		755		760		765
Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln Val Ala Asn						
		770		775		780
Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu Val Ala Ala						
		785		790		800

Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu Ala Val Pro Leu
805 810 815

Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu Ser Ala Lys Gly His
820 825 830

His His His His His
835

<210> 2836

<211> 2493

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 2836

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cagatggtct acggcttcgc ccggagcctc ctcaaggccc tcaaggagga cggggacgcg	180
gtgatcgtgg tctttgacgc cgaggccccc tccttcgcgc accagacctt cgaggcctac	240
aaggcgggga gggctccac ccccgaggac tttccccggc agcttgccct tatcaaggag	300
ctggtggacc tcctgggggtt taccgcctc gaggtccccg gctacgaggc ggacgacgtt	360
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aagacggcga ggaagcttct ggaggagtgg gggagcctgg aagccctcct caagaacctg	660
gaccgggtga agcccgccat ccgggagaag atcctggccc acatggacga tctgaagctc	720
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ctccacgagt tcggcccttt ggaaagcccc agggccgcgg aggaagctcc ctggccgccc	900
cccaggggag ccttcgtggg gtacgttctt tcccgccccg agcccatgtg ggcggagctt	960
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gccgcccacc gggccctcct ctcgagagag ctccatcgga acctccttaa gcgcctcgag	1260
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caggtcgcca acgagctcct cctggaggcc cccaagcgc gggccgagga ggtggcggt	2400
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<210> 2837

<211> 831

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 2837

Met Asn Ser Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu Val
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Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu Lys Gly Leu
20 25 30

Thr Thr Ser Arg Gly Glu Pro Val Gln Met Val Tyr Gly Phe Ala Arg
35 40 45

Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile Val Val
50 55 60

Phe Asp Ala Glu Ala Pro Ser Phe Arg His Gln Thr Tyr Glu Ala Tyr
65 70 75 80

Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu Ala
85 90 95

Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr Arg Leu Glu Val
100 105 110

Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu Ala Lys Lys Ala
115 120 125

Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Arg Asp Leu
130 135 140

Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu Gly Tyr
145 150 155 160

Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg Pro Asp
165 170 175

Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp Asn Leu
180 185 190

Ser Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu Leu Glu
195 200 205

Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg Leu Lys
210 215 220

Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu Lys Leu
225 230 235 240

Ser Leu Glu Leu Ser Arg Val Arg Thr Asp Leu Pro Leu Glu Val Asp
 245 250 255
 Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala Phe Leu
 260 265 270
 Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Pro Leu Glu
 275 280 285
 Ser Pro Arg Ala Ala Glu Glu Ala Pro Trp Pro Pro Pro Glu Gly Ala
 290 295 300
 Phe Val Gly Tyr Val Leu Ser Arg Pro Glu Pro Met Trp Ala Glu Leu
 305 310 315 320
 Asn Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala Ala Asp
 325 330 335
 Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly Leu Leu Ala
 340 345 350
 Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp Leu Val Pro
 355 360 365
 Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Gly Pro Ser Asn Thr
 370 375 380
 Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu Asp
 385 390 395 400
 Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg Asn Leu Leu
 405 410 415
 Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr His Glu Val
 420 425 430
 Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr Gly Val
 435 440 445
 Arg Leu Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu Leu Ala Glu
 450 455 460
 Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala Gly His Pro
 465 470 475 480
 Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe Asp Glu
 485 490 495

Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys Thr Gly Lys Arg Ser
 500 505 510

Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro Ile Val
 515 520 525

Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys Asn Thr Tyr
 530 535 540

Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly Arg Leu His
 545 550 555 560

Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser Ser
 565 570 575

Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly Gln Arg
 580 585 590

Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu Val Ala Leu
 595 600 605

Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly Asp
 610 615 620

Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp Ile His Thr Gln
 625 630 635 640

Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val Asp Pro Leu
 645 650 655

Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu Tyr Gly Met
 660 665 670

Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu Glu Ala
 675 680 685

Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val Arg Ala
 690 695 700

Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly Tyr Val Glu
 705 710 715 720

Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn Ala Arg Val
 725 730 735

Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro Val

	740		745		750	
Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys Leu Phe						
	755		760		765	
Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln Val Ala Asn						
	770		775		780	
Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu Val Ala Ala						
	785		790		795	800
Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu Ala Val Pro Leu						
		805		810		815
Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu Ser Ala Lys Gly						
		820		825		830

<210> 2838

<211> 2526

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 2838

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gaaccggtgc aggcggtcta cggcttcgcc aagagcctcc tcaaggccct gaaggaggac	180
gggtacaagg ccgtcttcgt ggtctttgac gccaaggccc cctccttcgg ccacgaggcc	240
tacgaggcct acaaggcggg gagggccccg acccccgagg acttcccccg gcagctcgcc	300
ctcatcaagg agctggtgga cctcctgggg tttaccgcgc tcgaggtccc cggctacgag	360
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atcctcaccg ccgaccgcga cctctaccaa ctcgctctccg accgcgtcgc cgtcctccac	480
cccgagggcc acctcatcac cccggagtgg ctttgggaga agtacggcct caggccggag	540
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gagttcggca	gcctcctcca	cgagttcggc	ctcctggagg	cccccgcccc	cctggaggag	900
gccccctggc	ccccgcccga	aggggccttc	gtgggcttcg	tcctctcccc	ccccgagccc	960
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gccgtcttgg	cctcgaggga	ggggctagac	ctcgtgcccc	gggacgaccc	catgctcctc	1140
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caccac						2526

<210> 2839

<211> 842

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 2839

Met Asn Ser Glu Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val
1 5 10 15

Leu Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu
20 25 30

Lys Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly
35 40 45

Phe Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Tyr Lys Ala
50 55 60

Val Phe Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala
65 70 75 80

Tyr Glu Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro
85 90 95

Arg Gln Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr
100 105 110

Arg Leu Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu
115 120 125

Ala Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala
130 135 140

Asp Arg Asp Leu Tyr Gln Leu Val Ser Asp Arg Val Ala Val Leu His
145 150 155 160

Pro Glu Gly His Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly
165 170 175

Leu Arg Pro Glu Gln Trp Val Asp Phe Arg Ala Leu Val Gly Asp Pro
180 185 190

Ser Asp Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu
 195 200 205

Lys Leu Leu Lys Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu
 210 215 220

Asp Arg Val Lys Pro Glu Asn Val Arg Glu Lys Ile Lys Ala His Leu
 225 230 235 240

Glu Asp Leu Arg Leu Ser Leu Glu Leu Ser Arg Val Arg Thr Asp Leu
 245 250 255

Pro Leu Glu Val Asp Leu Ala Gln Gly Arg Glu Pro Asp Arg Glu Gly
 260 265 270

Leu Arg Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu
 275 280 285

Phe Gly Leu Leu Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro
 290 295 300

Pro Pro Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro
 305 310 315 320

Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val
 325 330 335

His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val
 340 345 350

Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly
 355 360 365

Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu
 370 375 380

Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly
 385 390 395 400

Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu
 405 410 415

His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp
 420 425 430

Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met

435	440	445
Glu Ala Thr Gly Val Arg	Leu Asp Val Ala Tyr	Leu Gln Ala Leu Ser
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Leu Glu Leu Ala Glu Glu Ile Arg Arg	Leu Glu Glu Glu Val Phe Arg	
465	470	475
Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg		
485	490	495
Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys		
500	505	510
Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu		
515	520	525
Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys		
530	535	540
Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg		
545	550	555
Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly		
565	570	575
Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr		
580	585	590
Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp		
595	600	605
Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala		
610	615	620
His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys		
625	630	635
Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu		
645	650	655
Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly		
660	665	670
Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile		
675	680	685

Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe
690 695 700

Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys
705 710 715 720

Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp
725 730 735

Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala
740 745 750

Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala
755 760 765

Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu
770 775 780

Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala
785 790 795 800

Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro
805 810 815

Leu Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu
820 825 830

Ser Ala Lys Gly His His His His His His
835 840

<210> 2840

<211> 2526

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 2840

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gaaccggtgc aggcggtcta cggcttcgcc aagagcctcc tcaaggccct gaaggaggac 180

gggtacaagg ccgtcttcgt ggtctttgac gccaaaggccc cctccttcgg ccacgaggcc 240

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ctcatcaagg	agctggtgga	cctcctgggg	tttaccgcgc	tcgaggtccc	cggtctacgag	360
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cccagggggc	acctcatcac	cccggagtgg	ctttgggaga	agtacggcct	caggccggag	540
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 caccac 2526

<210> 2841

<211> 842

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 2841

Met Asn Ser Glu Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val
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Leu Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu
 20 25 30

Lys Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly
 35 40 45

Phe Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Tyr Lys Ala
 50 55 60

Val Phe Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala
 65 70 75 80

Tyr Glu Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro
 85 90 95

Arg Gln Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr
 100 105 110

Arg Leu Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu

115					120					125					
Ala	Lys	Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala
130						135					140				
Asp	Arg	Asp	Leu	Tyr	Gln	Leu	Val	Ser	Asp	Arg	Val	Ala	Val	Leu	His
145					150					155					160
Pro	Glu	Gly	His	Leu	Ile	Thr	Pro	Glu	Trp	Leu	Trp	Glu	Lys	Tyr	Gly
				165					170					175	
Leu	Arg	Pro	Glu	Gln	Trp	Val	Asp	Phe	Arg	Ala	Leu	Val	Gly	Asp	Pro
			180					185					190		
Ser	Asp	Asn	Leu	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Leu
		195					200					205			
Lys	Leu	Leu	Lys	Glu	Trp	Gly	Ser	Leu	Glu	Asn	Leu	Leu	Lys	Asn	Leu
	210					215					220				
Asp	Arg	Val	Lys	Pro	Glu	Asn	Val	Arg	Glu	Lys	Ile	Lys	Ala	His	Leu
225					230					235					240
Glu	Asp	Leu	Arg	Leu	Ser	Leu	Glu	Leu	Ser	Arg	Val	Arg	Thr	Asp	Leu
				245					250					255	
Pro	Leu	Glu	Val	Asp	Leu	Ala	Gln	Gly	Arg	Glu	Pro	Asp	Arg	Glu	Gly
			260					265					270		
Leu	Arg	Ala	Phe	Leu	Glu	Arg	Leu	Glu	Phe	Gly	Ser	Leu	Leu	His	Glu
		275					280					285			
Phe	Gly	Leu	Leu	Glu	Ala	Pro	Ala	Pro	Leu	Glu	Glu	Ala	Pro	Trp	Pro
	290					295					300				
Pro	Pro	Glu	Gly	Ala	Phe	Val	Gly	Phe	Val	Leu	Ser	Arg	Pro	Glu	Pro
305					310					315				320	
Met	Trp	Ala	Glu	Leu	Lys	Ala	Leu	Ala	Ala	Cys	Arg	Gly	Gly	Arg	Val
				325					330					335	
His	Arg	Ala	Ala	Asp	Pro	Leu	Ala	Gly	Leu	Lys	Asp	Leu	Lys	Glu	Val
			340					345					350		
Arg	Gly	Leu	Leu	Ala	Lys	Asp	Leu	Ala	Val	Leu	Ala	Ser	Arg	Glu	Gly
		355					360					365			

Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu
 370 375 380

Gly Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly
 385 390 395 400

Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu
 405 410 415

His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp
 420 425 430

Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met
 435 440 445

Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser
 450 455 460

Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg
 465 470 475 480

Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg
 485 490 495

Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys
 500 505 510

Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu
 515 520 525

Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys
 530 535 540

Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg
 545 550 555 560

Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly
 565 570 575

Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr
 580 585 590

Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp
 595 600 605

Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala
 610 615 620

His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys
625 630 635 640

Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu
645 650 655

Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly
660 665 670

Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile
675 680 685

Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe
690 695 700

Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys
705 710 715 720

Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp
725 730 735

Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala
740 745 750

Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala
755 760 765

Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu
770 775 780

Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala
785 790 795 800

Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro
805 810 815

Leu Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu
820 825 830

Ser Ala Lys Gly His His His His His His
835 840

<210> 2842

<211> 2526

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 2842

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gaaccggtgc aggcggtcta cggcttcgcc aagagcctcc tcaaggccct gaaggaggac      180
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<210> 2843

<211> 842

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 2843

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Met Asn Ser Glu Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val
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Leu Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu
          20          25          30

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```

Lys Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly
35          40          45

```

```

Phe Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Tyr Lys Ala

```

50	55	60
Val Phe Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala 65 70 75 80		
Tyr Glu Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro 85 90 95		
Arg Gln Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr 100 105 110		
Arg Leu Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu 115 120 125		
Ala Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala 130 135 140		
Asp Arg Asp Leu Tyr Gln Leu Val Ser Asp Arg Val Ala Val Leu His 145 150 155 160		
Pro Glu Gly His Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly 165 170 175		
Leu Arg Pro Glu Gln Trp Val Asp Phe Arg Ala Leu Val Gly Asp Pro 180 185 190		
Ser Asp Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu 195 200 205		
Lys Leu Leu Lys Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu 210 215 220		
Asp Arg Val Lys Pro Glu Asn Val Arg Glu Lys Ile Lys Ala His Leu 225 230 235 240		
Glu Asp Leu Arg Leu Ser Leu Glu Leu Ser Arg Val Arg Thr Asp Leu 245 250 255		
Pro Leu Glu Val Asp Leu Ala Gln Gly Arg Glu Pro Asp Arg Glu Gly 260 265 270		
Leu Arg Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu 275 280 285		
Phe Gly Leu Leu Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro 290 295 300		

Pro Pro Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro
 305 310 315 320
 Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val
 325 330 335
 His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val
 340 345 350
 Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly
 355 360 365
 Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu
 370 375 380
 Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly
 385 390 395 400
 Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu
 405 410 415
 His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp
 420 425 430
 Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met
 435 440 445
 Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser
 450 455 460
 Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg
 465 470 475 480
 Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg
 485 490 495
 Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys
 500 505 510
 Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu
 515 520 525
 Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys
 530 535 540
 Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg
 545 550 555 560

Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly
 565 570 575

Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr
 580 585 590

Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp
 595 600 605

Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala
 610 615 620

His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys
 625 630 635 640

Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu
 645 650 655

Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly
 660 665 670

Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile
 675 680 685

Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe
 690 695 700

Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys
 705 710 715 720

Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp
 725 730 735

Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala
 740 745 750

Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala
 755 760 765

Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu
 770 775 780

Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala
 785 790 795 800

Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro

	805		810		815										
Leu	Ala	Val	Pro	Leu	Glu	Val	Glu	Val	Gly	Met	Gly	Glu	Asp	Trp	Leu
			820						825				830		
Ser	Ala	Lys	Gly	His	His	His	His	His	His						
		835					840								

<210> 2844

<211> 2526

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 2844

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gaaccggtgc aggcggtcta cggcttcgcc aagagcctcc tcaaggccct gaaggaggac	180
gggtacaagg ccgtcttcgt ggtctttgac gccaaaggccc cctccttcgc ccacgaggcc	240
tacgaggcct acaaggcggg gagggccccg acccccgagg acttccccgc gcagctcgcc	300
ctcatcaagg agctggtgga cctcctgggg tttaccgcgc tcgaggctcc cggctacgag	360
gcggacgacg ttctcgccac cctggccaag aaggcggaag aggaggggta cgagggtcgc	420
atcctcaccg ccgaccgcga cctctaccaa ctcgctctcc accgcgtcgc cgtcctccac	480
cccgagggcc acctcatcac cccggagtgg ctttgggaga agtacggcct caggccggag	540
cagtgggtgg acttccgcgc cctcgtgggg gacccctccg acaacctccc cggggtcaag	600
ggcatcgggg agaagaccgc cctcaagctc ctcaaggagt ggggaagcct ggaaaacctc	660
ctcaagaacc tggaccgggt aaagccagaa aacgtccggg agaagatcaa ggcccacctg	720
gaagacctca ggctctcctt ggagctctcc cgggtgcgca ccgacctccc cctggagggtg	780
gacctcggcc aggggcggga gcccgaaccg gaggggctta gggccttcct ggagaggctg	840
gagttcggca gcctcctcca cgagttcggc ctctggagg ccccgcccc cctggaggag	900
gccccctggc ccccgccgga aggggccttc gtgggcttcg tcctctcccg ccccgagccc	960
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gaccccttgg cggggctaaa ggacctcaag gaggtccggg gcctcctcgc caaggacctc	1080

gccgtcttgg cctcgaggga ggggctagac ctctgtcccc gggacgaccc catgctcctc	1140
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gagtggacgg aggacgccc ccaccggggc ctctctctcg agaggctcca tcggaacctc	1260
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gagcttaggc ttccgcctt gaagaagacg aagaagacag gcaagcgctc caccagcgcc	1560
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gaggagggtg cggctttggc caaggaggcc atggagaagg cctatcccc cgcgtgccc	2460
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caccac	2526

<210> 2845

<211> 842

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 2845

Met Asn Ser Glu Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val
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Leu Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Arg Phe Ala Leu
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Lys Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly
35 40 45

Phe Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Tyr Lys Ala
50 55 60

Val Phe Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala
65 70 75 80

Tyr Glu Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro
85 90 95

Arg Gln Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr
100 105 110

Arg Leu Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu
115 120 125

Ala Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala
130 135 140

Asp Arg Asp Leu Tyr Gln Leu Val Ser Asp Arg Val Ala Val Leu His
145 150 155 160

Pro Glu Gly His Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly
165 170 175

Leu Arg Pro Glu Gln Trp Val Asp Phe Arg Ala Leu Val Gly Asp Pro
180 185 190

Ser Asp Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu
195 200 205

Lys Leu Leu Lys Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu
210 215 220

Asp Arg Val Lys Pro Glu Asn Val Arg Glu Lys Ile Lys Ala His Leu
225 230 235 240

485										490					495				
Val	Leu	Phe	Asp	Glu	Leu	Arg	Leu	Pro	Ala	Leu	Lys	Lys	Thr	Lys	Lys				
			500					505					510						
Thr	Gly	Lys	Arg	Ser	Thr	Ser	Ala	Ala	Val	Leu	Glu	Ala	Leu	Arg	Glu				
		515					520					525							
Ala	His	Pro	Ile	Val	Glu	Lys	Ile	Leu	Gln	His	Arg	Glu	Leu	Thr	Lys				
	530					535					540								
Leu	Lys	Asn	Thr	Tyr	Val	Asp	Pro	Leu	Pro	Ser	Leu	Val	His	Pro	Arg				
545					550					555					560				
Thr	Gly	Arg	Leu	His	Thr	Arg	Phe	Asn	Gln	Thr	Ala	Thr	Ala	Thr	Gly				
				565					570						575				
Arg	Leu	Ser	Ser	Ser	Asp	Pro	Asn	Leu	Gln	Asn	Ile	Pro	Val	Arg	Thr				
			580					585					590						
Pro	Leu	Gly	Gln	Arg	Ile	Arg	Arg	Ala	Phe	Val	Ala	Glu	Ala	Gly	Trp				
		595					600					605							
Ala	Leu	Val	Ala	Leu	Asp	Tyr	Ser	Gln	Ile	Glu	Leu	Arg	Val	Leu	Ala				
	610					615					620								
His	Leu	Ser	Gly	Asp	Glu	Asn	Leu	Ile	Arg	Val	Phe	Gln	Glu	Gly	Lys				
625					630					635					640				
Asp	Ile	His	Thr	Gln	Thr	Ala	Ser	Trp	Met	Phe	Gly	Val	Pro	Pro	Glu				
				645					650					655					
Ala	Val	Asp	Pro	Leu	Met	Arg	Arg	Ala	Ala	Lys	Thr	Val	Asn	Phe	Gly				
			660					665					670						
Val	Leu	Tyr	Gly	Met	Ser	Ala	His	Arg	Leu	Ser	Gln	Glu	Leu	Ala	Ile				
		675					680					685							
Pro	Tyr	Glu	Glu	Ala	Val	Ala	Phe	Ile	Glu	Arg	Tyr	Phe	Gln	Ser	Phe				
	690					695					700								
Pro	Lys	Val	Arg	Ala	Trp	Ile	Glu	Lys	Thr	Leu	Glu	Glu	Gly	Arg	Lys				
705					710					715					720				
Arg	Gly	Tyr	Val	Glu	Thr	Leu	Phe	Gly	Arg	Arg	Arg	Tyr	Val	Pro	Asp				
				725					730					735					

Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala
740 745 750

Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala
755 760 765

Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu
770 775 780

Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala
785 790 795 800

Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro
805 810 815

Leu Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu
820 825 830

Ser Ala Lys Gly His His His His His His
835 840

<210> 2846

<211> 2526

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 2846

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gaaccggtgc aggcggtcta cggtctcgcc aagagcctcc tcaaggccct gaaggaggac	180
gggtacaagg ccgtcttcgt ggtctttgac gccaaaggccc cctccttcg ccacgaggcc	240
tacgaggcct acaaggcggg gagggccccg acccccgagg acttccccg gcagctcgcc	300
ctcatcaagg agctggtgga cctcctgggg tttaccgcgc tcgaggtccc cggctacgag	360
gcggacgacg ttctcgccac cctggccaag aaggcggaaa aggaggggta cgaggtgcgc	420
atcctcaccg ccgaccgcga cctctaccaa ctcgctctccg accgcgtcgc cgtcctccac	480
cccagaggcc acctcatcac cccggagtgg ctttgggaga agtacggcct caggccggag	540
cagtgggtgg acttccgcgc cctcgtgggg gaccctccg acaacctccc cgggggtcaag	600

ggcatcgggg	agaagaccgc	cctcaagctc	ctcaaggagt	ggggaagcct	ggaaaacctc	660
ctcaagaacc	tggaccgggt	aaagccagaa	aacgtccggg	agaagatcaa	ggcccacctg	720
gaagacctca	ggctctcctt	ggagctctcc	cgggtgcgca	ccgacctccc	cctggagggtg	780
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gccgtcttgg	cctcgaggga	ggggctagac	ctcgtgcccc	gggacgaccc	catgctcctc	1140
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ctgatgcgcc	gggcggccaa	gacggtgaac	ttcggcgctc	tctacggcat	gtccgcccac	2040
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ttccaaagct	tccccaaggt	gcgggcctgg	atagaaaaga	ccctggagga	ggggaggaag	2160
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gcccgcacgc	tcctccaggt	cgccaacgag	ctcctcctgg	aggcccccca	agcgcgggcc	2400
gaggagggtg	cggctttggc	caaggaggcc	atggagaagg	cctatcccct	cgcctgtccc	2460

ctggagggtgg aggtgggggat gggggaggac tggctttccg ccaagggtca ccaccaccac 2520
caccac 2526

<210> 2847

<211> 842

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 2847

Met Asn Ser Glu Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val
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Leu Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Arg His Ala Leu
20 25 30

Lys Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly
35 40 45

Phe Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Tyr Lys Ala
50 55 60

Val Phe Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala
65 70 75 80

Tyr Glu Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro
85 90 95

Arg Gln Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr
100 105 110

Arg Leu Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu
115 120 125

Ala Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala
130 135 140

Asp Arg Asp Leu Tyr Gln Leu Val Ser Asp Arg Val Ala Val Leu His
145 150 155 160

Pro Glu Gly His Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly

His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp
420 425 430

Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met
435 440 445

Glu Ala Thr Gly Val Arg Leu Asp Val Ala Tyr Leu Gln Ala Leu Ser
450 455 460

Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg
465 470 475 480

Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg
485 490 495

Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys
500 505 510

Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu
515 520 525

Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys
530 535 540

Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg
545 550 555 560

Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly
565 570 575

Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr
580 585 590

Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp
595 600 605

Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala
610 615 620

His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys
625 630 635 640

Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu
645 650 655

Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly
660 665 670

Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile
675 680 685

Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe
690 695 700

Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys
705 710 715 720

Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp
725 730 735

Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala
740 745 750

Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala
755 760 765

Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu
770 775 780

Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala
785 790 795 800

Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro
805 810 815

Leu Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu
820 825 830

Ser Ala Lys Gly His His His His His His
835 840

<210> 2848

<211> 2526

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 2848

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gaaccggtgc	aggcggtcta	cggcttcgcc	aagagcctcc	tcaaggccct	gaaggaggac	180
gggtacaagg	ccgtcttcgt	ggtctttgac	gccaaggccc	cctccttcgg	ccacgaggcc	240
tacgaggcct	acaaggcggg	gagggccccc	accccgagg	acttcccccg	gcagctcgcc	300
ctcatcaagg	agctggtgga	cctcctgggg	tttaccgcgc	tgcaggtccc	cggctacgag	360
gcggacgacg	ttctcgccac	cctggccaag	aaggcggaaa	aggaggggta	cgaggtgcgc	420
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cagtgggtgg	acttccgcgc	cctcgtgggg	gaccctcccg	acaacctccc	cggggtaag	600
ggcatcgggg	agaagaccgc	cctcaagctc	ctcaaggagt	ggggaagcct	ggaaaacctc	660
ctcaagaacc	tggaccgggt	aaagccagaa	aacgtccggg	agaagatcaa	ggcccacctg	720
gaagacctca	ggctctcctt	ggagctctcc	cgggtgcgca	ccgacctccc	cctggagggtg	780
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gccttcgtgg	ccgaggcggg	ttgggcgttg	gtggccctgg	actatagcca	gatagagctc	1860
cgcgtcctcg	cccacctctc	cggggacgaa	aacctgatca	gggtcttcca	ggaggggaag	1920

gacatccaca cccagaccgc aagctggatg ttcggcgtcc ccccgagggc cgtggacccc 1980
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gaggaggtgg cggctttggc caaggaggcc atggagaagg cctatcccct cgccgtgccc 2460
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caccac 2526

<210> 2849

<211> 842

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 2849

Met Asn Ser Glu Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val
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Leu Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Arg Arg Ala Leu
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Lys Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly
35 40 45

Phe Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Tyr Lys Ala
50 55 60

Val Phe Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala
65 70 75 80

Tyr Glu Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro
85 90 95

Arg Gln Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr
 100 105 110

Arg Leu Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu
 115 120 125

Ala Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala
 130 135 140

Asp Arg Asp Leu Tyr Gln Leu Val Ser Asp Arg Val Ala Val Leu His
 145 150 155 160

Pro Glu Gly His Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly
 165 170 175

Leu Arg Pro Glu Gln Trp Val Asp Phe Arg Ala Leu Val Gly Asp Pro
 180 185 190

Ser Asp Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu
 195 200 205

Lys Leu Leu Lys Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu
 210 215 220

Asp Arg Val Lys Pro Glu Asn Val Arg Glu Lys Ile Lys Ala His Leu
 225 230 235 240

Glu Asp Leu Arg Leu Ser Leu Glu Leu Ser Arg Val Arg Thr Asp Leu
 245 250 255

Pro Leu Glu Val Asp Leu Ala Gln Gly Arg Glu Pro Asp Arg Glu Gly
 260 265 270

Leu Arg Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu
 275 280 285

Phe Gly Leu Leu Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro
 290 295 300

Pro Pro Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro
 305 310 315 320

Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val
 325 330 335

His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val
 340 345 350

Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly
 355 360 365

Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu
 370 375 380

Gly Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly
 385 390 395 400

Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu
 405 410 415

His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp
 420 425 430

Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met
 435 440 445

Glu Ala Thr Gly Val Arg Leu Asp Val Ala Tyr Leu Gln Ala Leu Ser
 450 455 460

Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg
 465 470 475 480

Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg
 485 490 495

Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys
 500 505 510

Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu
 515 520 525

Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys
 530 535 540

Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg
 545 550 555 560

Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly
 565 570 575

Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr
 580 585 590

Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp

595					600					605					
Ala	Leu	Val	Ala	Leu	Asp	Tyr	Ser	Gln	Ile	Glu	Leu	Arg	Val	Leu	Ala
610						615					620				
His	Leu	Ser	Gly	Asp	Glu	Asn	Leu	Ile	Arg	Val	Phe	Gln	Glu	Gly	Lys
625					630					635					640
Asp	Ile	His	Thr	Gln	Thr	Ala	Ser	Trp	Met	Phe	Gly	Val	Pro	Pro	Glu
				645					650					655	
Ala	Val	Asp	Pro	Leu	Met	Arg	Arg	Ala	Ala	Lys	Thr	Val	Asn	Phe	Gly
			660					665					670		
Val	Leu	Tyr	Gly	Met	Ser	Ala	His	Arg	Leu	Ser	Gln	Glu	Leu	Ala	Ile
		675					680					685			
Pro	Tyr	Glu	Glu	Ala	Val	Ala	Phe	Ile	Glu	Arg	Tyr	Phe	Gln	Ser	Phe
	690					695					700				
Pro	Lys	Val	Arg	Ala	Trp	Ile	Glu	Lys	Thr	Leu	Glu	Glu	Gly	Arg	Lys
705					710					715					720
Arg	Gly	Tyr	Val	Glu	Thr	Leu	Phe	Gly	Arg	Arg	Arg	Tyr	Val	Pro	Asp
				725					730					735	
Leu	Asn	Ala	Arg	Val	Lys	Ser	Val	Arg	Glu	Ala	Ala	Glu	Arg	Met	Ala
			740					745					750		
Phe	Asn	Met	Pro	Val	Gln	Gly	Thr	Ala	Ala	Asp	Leu	Met	Lys	Leu	Ala
		755					760					765			
Met	Val	Lys	Leu	Phe	Pro	Arg	Leu	Arg	Glu	Met	Gly	Ala	Arg	Met	Leu
	770					775					780				
Leu	Gln	Val	Ala	Asn	Glu	Leu	Leu	Leu	Glu	Ala	Pro	Gln	Ala	Arg	Ala
785					790					795					800
Glu	Glu	Val	Ala	Ala	Leu	Ala	Lys	Glu	Ala	Met	Glu	Lys	Ala	Tyr	Pro
				805					810					815	
Leu	Ala	Val	Pro	Leu	Glu	Val	Glu	Val	Gly	Met	Gly	Glu	Asp	Trp	Leu
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Ser	Ala	Lys	Gly	His	His	His	His	His	His						
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<210> 2850

<211> 2514

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 2850

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caggcgggtgt acgggtttgc caagagcctt ttgaaggcgc taagggaaga cggggatgtg      180
gtgatcgtgg tgtttgacgc caaggccccc tccttcgcgc accagacctt cgaggcctac      240
aaggcggggc gggctccac ccccgaggac tttcccgcgc agcttgccct tatcaaggag      300
atggtggacc ttttgggcct ggagcgcctc gaggtgccgg gctttgaagc ggatgacgtc      360
ctggctaccc tggccaagaa ggcggaaaag gaaggctacg aagtgcgcac cctcaccgcg      420
gaccgggacc tttaccagct tctttcggag cgaatctcca tccttcaccc ggaggggttac      480
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taccgggcct tggccgggga cccttcgcgc aacatccccg gcgtgaaggg catcggggag      600
aagacggcgg ccaagctgat ccgggagtgg ggaagcctgg aaaaccttct taagcacctg      660
gaacaggtga aacctgcctc cgtgcgggag aagatcctta gccacatgga ggacctcaag      720
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gacgccgcc accgggccct cctctcggag aggtccatc ggaacctcct taagcgcctc     1260
gagggggagg agaagctcct ttggctctac cacgaggtgg aaaagcccct ctcccgggtc     1320
ctggcccaca tggaggccac cggggtacgg ctggacgtgg cctaccttca ggccctttcc     1380
ctggagcttg cggaggagat ccgccgcctc gaggaggagg tcttccgctt ggccggccac     1440
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cacacccgct tcaaccagac ggccacggcc acggggaggc ttagtagctc cgaccccaac 1740
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gctttggcca aggaggccat ggagaaggcc tatccctcgc ccgtgcccct ggagggtggag 2460
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<210> 2851

<211> 838

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 2851

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Met Asn Ser Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu Val
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Asp Gly His His Leu Ala Tyr Arg Thr Arg Phe Ala Leu Lys Gly Leu
          20          25          30

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Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala Lys

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Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Gln	Thr	Tyr	Glu	Ala	Tyr
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Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln	Leu	Ala
				85					90					95	
Leu	Ile	Lys	Glu	Met	Val	Asp	Leu	Leu	Gly	Leu	Glu	Arg	Leu	Glu	Val
			100					105					110		
Pro	Gly	Phe	Glu	Ala	Asp	Asp	Val	Leu	Ala	Thr	Leu	Ala	Lys	Lys	Ala
		115					120					125			
Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	Arg	Asp	Leu
	130					135					140				
Tyr	Gln	Leu	Leu	Ser	Glu	Arg	Ile	Ser	Ile	Leu	His	Pro	Glu	Gly	Tyr
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Leu	Ile	Thr	Pro	Glu	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	Leu	Lys	Pro	Ser
				165					170					175	
Gln	Trp	Val	Asp	Tyr	Arg	Ala	Leu	Ala	Gly	Asp	Pro	Ser	Asp	Asn	Ile
			180				185						190		
Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Ala	Lys	Leu	Ile	Arg
		195					200					205			
Glu	Trp	Gly	Ser	Leu	Glu	Asn	Leu	Leu	Lys	His	Leu	Glu	Gln	Val	Lys
	210					215					220				
Pro	Ala	Ser	Val	Arg	Glu	Lys	Ile	Leu	Ser	His	Met	Glu	Asp	Leu	Lys
225					230					235					240
Leu	Ser	Leu	Glu	Leu	Ser	Arg	Val	His	Thr	Asp	Leu	Leu	Leu	Gln	Val
				245					250					255	
Asp	Phe	Ala	Arg	Arg	Arg	Glu	Pro	Asp	Arg	Glu	Gly	Leu	Lys	Ala	Phe
			260					265					270		
Leu	Glu	Arg	Leu	Glu	Phe	Gly	Ser	Leu	Leu	His	Glu	Phe	Gly	Leu	Leu
		275					280					285			

Glu Ser Pro Val Ala Ala Glu Glu Ala Pro Trp Pro Pro Pro Glu Gly
 290 295 300
 Ala Phe Val Gly Tyr Val Leu Ser Arg Pro Glu Pro Met Trp Ala Glu
 305 310 315 320
 Leu Asn Ala Leu Ala Ala Ala Trp Gly Gly Arg Val His Arg Ala Ala
 325 330 335
 Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly Leu Leu
 340 345 350
 Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp Leu Val
 355 360 365
 Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Gly Pro Ser Asn
 370 375 380
 Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu
 385 390 395 400
 Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg Asn Leu
 405 410 415
 Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr His Glu
 420 425 430
 Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr Gly
 435 440 445
 Val Arg Leu Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu Leu Ala
 450 455 460
 Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala Gly His
 465 470 475 480
 Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe Asp
 485 490 495
 Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys Thr Gly Lys Arg
 500 505 510
 Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro Ile
 515 520 525
 Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys Asn Thr
 530 535 540

Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly Arg Leu
 545 550 555 560

His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser
 565 570 575

Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly Gln
 580 585 590

Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu Val Ala
 595 600 605

Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly
 610 615 620

Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp Ile His Thr
 625 630 635 640

Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val Asp Pro
 645 650 655

Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu Tyr Gly
 660 665 670

Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu Glu
 675 680 685

Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val Arg
 690 695 700

Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly Tyr Val
 705 710 715 720

Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn Ala Arg
 725 730 735

Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro
 740 745 750

Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys Leu
 755 760 765

Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln Val Ala
 770 775 780

Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu Val Ala

785		790		795		800									
Ala	Leu	Ala	Lys	Glu	Ala	Met	Glu	Lys	Ala	Tyr	Pro	Leu	Ala	Val	Pro
				805					810					815	
Leu	Glu	Val	Glu	Val	Gly	Met	Gly	Glu	Asp	Trp	Leu	Ser	Ala	Lys	Gly
			820					825					830		
His	His	His	His	His	His										
			835												

<210> 2852

<211> 2514

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 2852

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caggcgggtgt	acgggtttgc	caagagcctt	ttgaaggcgc	taagggaaga	cggggatgtg	180
gtgatcgtgg	tgtttgacgc	caaggccccc	tccttcgcgc	accagaccta	cgaggcctac	240
aaggcggggc	gggctcccac	ccccgaggac	tttccccggc	agcttgccct	tatcaaggag	300
atggtggacc	ttttgggcct	ggagcgcctc	gaggtgccgg	gctttgaagc	ggatgacgtc	360
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cagaccgcaa gctggatggt cggcgctccc ccggaggccg tggaccccct gatgcgccgg	1980
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<210> 2853

<211> 838

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 2853

Met Asn Ser Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu Val
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Asp Gly His His Leu Ala Tyr Arg Thr Arg His Ala Leu Lys Gly Leu
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Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala Lys
35 40 45

Ser Leu Leu Lys Ala Leu Arg Glu Asp Gly Asp Val Val Ile Val Val
50 55 60

Phe Asp Ala Lys Ala Pro Ser Phe Arg His Gln Thr Tyr Glu Ala Tyr
65 70 75 80

Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu Ala
85 90 95

Leu Ile Lys Glu Met Val Asp Leu Leu Gly Leu Glu Arg Leu Glu Val
100 105 110

Pro Gly Phe Glu Ala Asp Asp Val Leu Ala Thr Leu Ala Lys Lys Ala
115 120 125

Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Arg Asp Leu
130 135 140

Tyr Gln Leu Leu Ser Glu Arg Ile Ser Ile Leu His Pro Glu Gly Tyr
145 150 155 160

Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly Leu Lys Pro Ser
165 170 175

Gln Trp Val Asp Tyr Arg Ala Leu Ala Gly Asp Pro Ser Asp Asn Ile
180 185 190

Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Ala Lys Leu Ile Arg
195 200 205

Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys His Leu Glu Gln Val Lys
210 215 220

Pro Ala Ser Val Arg Glu Lys Ile Leu Ser His Met Glu Asp Leu Lys
 225 230 235 240

Leu Ser Leu Glu Leu Ser Arg Val His Thr Asp Leu Leu Leu Gln Val
 245 250 255

Asp Phe Ala Arg Arg Arg Glu Pro Asp Arg Glu Gly Leu Lys Ala Phe
 260 265 270

Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu Leu
 275 280 285

Glu Ser Pro Val Ala Ala Glu Glu Ala Pro Trp Pro Pro Pro Glu Gly
 290 295 300

Ala Phe Val Gly Tyr Val Leu Ser Arg Pro Glu Pro Met Trp Ala Glu
 305 310 315 320

Leu Asn Ala Leu Ala Ala Ala Trp Gly Gly Arg Val His Arg Ala Ala
 325 330 335

Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly Leu Leu
 340 345 350

Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp Leu Val
 355 360 365

Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Gly Pro Ser Asn
 370 375 380

Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu
 385 390 395 400

Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg Asn Leu
 405 410 415

Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr His Glu
 420 425 430

Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr Gly
 435 440 445

Val Arg Leu Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu Leu Ala
 450 455 460

Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala Gly His
 465 470 475 480

Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe Asp
 485 490 495

Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys Thr Gly Lys Arg
 500 505 510

Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro Ile
 515 520 525

Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys Asn Thr
 530 535 540

Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly Arg Leu
 545 550 555 560

His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser
 565 570 575

Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly Gln
 580 585 590

Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu Val Ala
 595 600 605

Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly
 610 615 620

Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp Ile His Thr
 625 630 635 640

Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val Asp Pro
 645 650 655

Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu Tyr Gly
 660 665 670

Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu Glu
 675 680 685

Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val Arg
 690 695 700

Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly Tyr Val
 705 710 715 720

Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn Ala Arg

	725		730		735
Val Lys Ser	Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro				
	740		745		750
Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys Leu					
	755		760		765
Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln Val Ala					
	770		775		780
Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu Val Ala					
	785		790		795
Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu Ala Val Pro					
	805		810		815
Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu Ser Ala Lys Gly					
	820		825		830
His His His His His His					
	835				

<210> 2854

<211> 2514

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 2854

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caggcgggtgt acgggtttgc caagagcctt ttgaaggcgc taagggaaga cggggatgtg	180
gtgatcgtgg tgtttgacgc caaggccccc tccttcgcgc accagaccta cgaggcctac	240
aaggcggggc gggctcccac ccccgaggac tttccccggc agcttgccct tatcaaggag	300
atggtggacc ttttgggcct ggagcgcctc gaggtgccgc gctttgaagc ggatgacgtc	360
ctggctaccc tggccaagaa ggcggaaaag gaaggctacg aagtgcgcac cctcaccgcg	420
gaccgggacc tttaccagct tctttcggag cgaatctcca tccttcaccc ggagggttac	480

ctgatcaccc	cggagtggct	ttgggagaag	tatgggctta	agccttccca	gtgggtggac	540
taccgggcct	tggccgggga	cccttccgac	aacatccccg	gcgtgaaggg	catcggggag	600
aagacggcgg	ccaagctgat	ccgggagtgg	ggaagcctgg	aaaaccttct	taagcacctg	660
gaacaggtga	aacctgcctc	cgtgcgggag	aagatcctta	gccacatgga	ggacctcaag	720
ctatccctgg	agctatcccc	ggtgcacacg	gacttgctcc	ttcaggtgga	cttcgcccgg	780
cgccgggagc	cggaccggga	ggggcttaag	gccttttttg	agaggctgga	gttcggaagc	840
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ccccccgagg	gagccttcgt	ggggtacgtt	ctttcccgc	ccgagcccat	gtgggcggag	960
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gggctaaagg	acctcaagga	ggtccggggc	ctcctcgcca	aggacctcgc	cgtcttggcc	1080
tcgagggagg	ggctagacct	cgtgcccggg	gacgacccca	tgtcctcgc	ctacctctg	1140
ggcccccca	acaccacccc	cgagggggtg	gcgcggcgct	acggggggga	gtggacggag	1200
gacgccgccc	accgggccct	cctctcgag	aggctccatc	ggaacctcct	taagcgctc	1260
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ctggcccaca	tggaggccac	cggggtacgg	ctggacgtgg	cctaccttca	ggcccccttc	1380
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gcggccaaga	cggatgaactt	cggcgtcctc	tacggcatgt	ccgcccatag	gctctccag	2040
gagcttgcca	tcccctacga	ggaggcggtg	gcctttatag	agcgctactt	ccaaagcttc	2100
cccaagggtg	gggcctggat	agaaaagacc	ctggaggagg	ggaggaagcg	gggctacgtg	2160
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ctccaggtcg ccaacgagct cctcctggag gcccccaag cgcgggccga ggaggtggcg 2400
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gtggggatgg gggaggactg gctttccgcc aagggtcacc accaccacca ccac 2514

<210> 2855

<211> 838

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 2855

Met Asn Ser Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu Val
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Asp Gly His His Leu Ala Tyr Arg Thr Arg Arg Ala Leu Lys Gly Leu
20 25 30

Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala Lys
35 40 45

Ser Leu Leu Lys Ala Leu Arg Glu Asp Gly Asp Val Val Ile Val Val
50 55 60

Phe Asp Ala Lys Ala Pro Ser Phe Arg His Gln Thr Tyr Glu Ala Tyr
65 70 75 80

Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu Ala
85 90 95

Leu Ile Lys Glu Met Val Asp Leu Leu Gly Leu Glu Arg Leu Glu Val
100 105 110

Pro Gly Phe Glu Ala Asp Asp Val Leu Ala Thr Leu Ala Lys Lys Ala
115 120 125

Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Arg Asp Leu
130 135 140

Tyr Gln Leu Leu Ser Glu Arg Ile Ser Ile Leu His Pro Glu Gly Tyr
145 150 155 160

Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly Leu Lys Pro Ser
165 170 175

Gln Trp Val Asp Tyr Arg Ala Leu Ala Gly Asp Pro Ser Asp Asn Ile
180 185 190

Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Ala Lys Leu Ile Arg
195 200 205

Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys His Leu Glu Gln Val Lys
210 215 220

Pro Ala Ser Val Arg Glu Lys Ile Leu Ser His Met Glu Asp Leu Lys
225 230 235 240

Leu Ser Leu Glu Leu Ser Arg Val His Thr Asp Leu Leu Leu Gln Val
245 250 255

Asp Phe Ala Arg Arg Arg Glu Pro Asp Arg Glu Gly Leu Lys Ala Phe
260 265 270

Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu Leu
275 280 285

Glu Ser Pro Val Ala Ala Glu Glu Ala Pro Trp Pro Pro Pro Glu Gly
290 295 300

Ala Phe Val Gly Tyr Val Leu Ser Arg Pro Glu Pro Met Trp Ala Glu
305 310 315 320

Leu Asn Ala Leu Ala Ala Ala Trp Gly Gly Arg Val His Arg Ala Ala
325 330 335

Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly Leu Leu
340 345 350

Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp Leu Val
355 360 365

Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Gly Pro Ser Asn
370 375 380

Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu
385 390 395 400

Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg Asn Leu
405 410 415

Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr His Glu
420 425 430

Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr Gly
435 440 445

Val Arg Leu Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu Leu Ala
450 455 460

Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala Gly His
465 470 475 480

Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe Asp
485 490 495

Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys Thr Gly Lys Arg
500 505 510

Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro Ile
515 520 525

Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys Asn Thr
530 535 540

Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly Arg Leu
545 550 555 560

His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser
565 570 575

Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly Gln
580 585 590

Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu Val Ala
595 600 605

Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly
610 615 620

Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp Ile His Thr
625 630 635 640

Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val Asp Pro
645 650 655

Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu Tyr Gly

660					665					670					
Met	Ser	Ala	His	Arg	Leu	Ser	Gln	Glu	Leu	Ala	Ile	Pro	Tyr	Glu	Glu
		675					680					685			
Ala	Val	Ala	Phe	Ile	Glu	Arg	Tyr	Phe	Gln	Ser	Phe	Pro	Lys	Val	Arg
	690					695					700				
Ala	Trp	Ile	Glu	Lys	Thr	Leu	Glu	Glu	Gly	Arg	Lys	Arg	Gly	Tyr	Val
705					710					715					720
Glu	Thr	Leu	Phe	Gly	Arg	Arg	Arg	Tyr	Val	Pro	Asp	Leu	Asn	Ala	Arg
				725					730					735	
Val	Lys	Ser	Val	Arg	Glu	Ala	Ala	Glu	Arg	Met	Ala	Phe	Asn	Met	Pro
			740					745					750		
Val	Gln	Gly	Thr	Ala	Ala	Asp	Leu	Met	Lys	Leu	Ala	Met	Val	Lys	Leu
		755					760					765			
Phe	Pro	Arg	Leu	Arg	Glu	Met	Gly	Ala	Arg	Met	Leu	Leu	Gln	Val	Ala
	770					775					780				
Asn	Glu	Leu	Leu	Leu	Glu	Ala	Pro	Gln	Ala	Arg	Ala	Glu	Glu	Val	Ala
785					790					795					800
Ala	Leu	Ala	Lys	Glu	Ala	Met	Glu	Lys	Ala	Tyr	Pro	Leu	Ala	Val	Pro
				805					810					815	
Leu	Glu	Val	Glu	Val	Gly	Met	Gly	Glu	Asp	Trp	Leu	Ser	Ala	Lys	Gly
			820					825					830		
His	His	His	His	His	His										
			835												

<210> 2856

<211> 2517

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 2856

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ccggtgcagg cggctctacgg cttcgccaag agcctcctca aggccctcaa ggaggacggg	180
gacgcggtga tcgtggtctt tgacgccaag gccccctcct tccgccacga ggccctacggg	240
gggtacaagg cgggccgggc cccacgcgcg gaggactttc cccggcaact cgccctcatc	300
aaggagctgg tggacctcct ggggctggcg cgcctcgagg tcccgggcta cgaggcggac	360
gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcctcctc	420
accgccgaca aagaccttta ccagctcctt tccgaccgca tccacgtcct ccaccccgag	480
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gccgactacc gggccctgac cggggacgag tccgacaacc ttcccggggg caagggcatc	600
ggggagaaga cggcgaggaa gcttctggag gagtggggga gcctggaagc cctcctcaag	660
aacctggacc ggctgaagcc cgccatccgg gagaagatcc tggcccacat ggacgatctg	720
aagctctcct gggacctggc caagggtgcg accgacctgc ccctggaggt ggacttcgcc	780
aaaaggcggg agcccgaccg ggagaggctt agggcctttc tggagaggct tgagtttggc	840
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gatcttctgg ccctggccgc cgccaggggc ggccgcgtgc accgggcagc agacccttg	1020
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cttcccgctt tgaagaagac gaagaagaca ggcaagcgct ccaccagcgc cgcggtgctg	1560
gaggccctac gggaggccca ccccatcggt gagaagatcc tccagcaccg ggagctcacc	1620
aagctcaaga acacctacgt ggacccccct ccaagcctcg tccaccgag gacgggccgc	1680
ctccacaccc gcttcaacca gacggccacg gccacgggga ggcttagtag ctccgacccc	1740
aacctgcaga acatccccgt ccgcaccccc ttggggcaga ggatccgccg ggccttcgtg	1800
gccgaggcgg gttgggcgtt ggtggccctg gactatagcc agatagagct ccgcgtcctc	1860

gccacacctt ccggggacga aaacctgac agggctcttc agggaggggaa ggacatccac 1920
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<210> 2857

<211> 839

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 2857

Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu
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Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Arg His Ala Leu Lys
 20 25 30

Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe
 35 40 45

Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile
 50 55 60

Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly
 65 70 75 80

Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln
 85 90 95

Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu
 100 105 110

Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys
 115 120 125

Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys
 130 135 140

Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu
 145 150 155 160

Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg
 165 170 175

Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp
 180 185 190

Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu
 195 200 205

Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg
 210 215 220

Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu
 225 230 235 240

Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu
 245 250 255

Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala
 260 265 270

Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu
 275 280 285

Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu
 290 295 300

Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala
 305 310 315 320

Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala
 325 330 335

Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly Leu
 340 345 350

Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp Leu
355 360 365

Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Gly Pro Ser
370 375 380

Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr
385 390 395 400

Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg Asn
405 410 415

Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr His
420 425 430

Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr
435 440 445

Gly Val Arg Leu Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu Leu
450 455 460

Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala Gly
465 470 475 480

His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe
485 490 495

Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys Thr Gly Lys
500 505 510

Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro
515 520 525

Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys Asn
530 535 540

Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly Arg
545 550 555 560

Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser
565 570 575

Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly
580 585 590

Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu Val

595					600					605					
Ala	Leu	Asp	Tyr	Ser	Gln	Ile	Glu	Leu	Arg	Val	Leu	Ala	His	Leu	Ser
610						615					620				
Gly	Asp	Glu	Asn	Leu	Ile	Arg	Val	Phe	Gln	Glu	Gly	Lys	Asp	Ile	His
625					630					635					640
Thr	Gln	Thr	Ala	Ser	Trp	Met	Phe	Gly	Val	Pro	Pro	Glu	Ala	Val	Asp
				645					650					655	
Pro	Leu	Met	Arg	Arg	Ala	Ala	Lys	Thr	Val	Asn	Phe	Gly	Val	Leu	Tyr
			660					665					670		
Gly	Met	Ser	Ala	His	Arg	Leu	Ser	Gln	Glu	Leu	Ala	Ile	Pro	Tyr	Glu
		675					680					685			
Glu	Ala	Val	Ala	Phe	Ile	Glu	Arg	Tyr	Phe	Gln	Ser	Phe	Pro	Lys	Val
	690					695					700				
Arg	Ala	Trp	Ile	Glu	Lys	Thr	Leu	Glu	Glu	Gly	Arg	Lys	Arg	Gly	Tyr
705					710					715					720
Val	Glu	Thr	Leu	Phe	Gly	Arg	Arg	Arg	Tyr	Val	Pro	Asp	Leu	Asn	Ala
				725					730					735	
Arg	Val	Lys	Ser	Val	Arg	Glu	Ala	Ala	Glu	Arg	Met	Ala	Phe	Asn	Met
			740					745					750		
Pro	Val	Gln	Gly	Thr	Ala	Ala	Asp	Leu	Met	Lys	Leu	Ala	Met	Val	Lys
		755					760					765			
Leu	Phe	Pro	Arg	Leu	Arg	Glu	Met	Gly	Ala	Arg	Met	Leu	Leu	Gln	Val
	770					775					780				
Ala	Asn	Glu	Leu	Leu	Leu	Glu	Ala	Pro	Gln	Ala	Arg	Ala	Glu	Glu	Val
785					790					795					800
Ala	Ala	Leu	Ala	Lys	Glu	Ala	Met	Glu	Lys	Ala	Tyr	Pro	Leu	Ala	Val
				805					810					815	
Pro	Leu	Glu	Val	Glu	Val	Gly	Met	Gly	Glu	Asp	Trp	Leu	Ser	Ala	Lys
			820					825					830		
Gly	His	His	His	His	His	His									
		835													

<210> 2858
 <211> 31
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic
 <400> 2858
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 <210> 2859
 <211> 31
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic
 <400> 2859
 ggtggtgttc gaagggtcca ggaggtaggc g 31

 <210> 2860
 <211> 28
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic
 <400> 2860
 ggtacggcgg gacgtggcct accttcag 28

 <210> 2861
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic
 <400> 2861
 ctgaaggtag gccacgtccc gccgtacc 28

<210> 2862
 <211> 39
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic
 <400> 2862
 cacctggcct accgcacccg cttcgccctg aagggcctc 39

<210> 2863
 <211> 39
 <212> DNA
 <213> Artificial Sequence

<220>
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23

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25

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17

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23

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20

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19

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14

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21

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22

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17

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15

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18

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17

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23

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20

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 gtcttagacc tgcgagcc

18

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caaggaagca gtgatc

16

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cctcccggcg ctttcga

17

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agcctcaaga tcacgtgat ct

22

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<223> The residue at this position is linked to a Z28 quenching group.

<400> 3157
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<210> 3158
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<220>
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<400> 3158
cactgcttcg tgg 13

<210> 3159
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<220>
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<400> 3159

ccaggaagca agtggatgac tcggcggc

28

<210> 3160

<211> 14

<212> DNA

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<220>

<223> Synthetic

<220>

<221> misc_feature

<222> (3)..(3)

<223> The residue at this position is linked to a Z28 quenching group.

<400> 3160

ctcttctcag tgcg

14

<210> 3161

<211> 14

<212> DNA

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<220>

<223> Synthetic

<220>

<221> misc_feature

<222> (3)..(3)

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14

<210> 3162

<211> 13

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 <210> 3163
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 <220>
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 <220>
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 <223> The residue at this position is linked to a Z28 quenching group.

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 tccactccga gct 13

 <210> 3164
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<220>
 <223> Synthetic
 <400> 3164
 agctcggagt aggagtgcgc ctcgttt 27

 <210> 3165
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 agcacggagt aggagtgcgc ctcgttt 27

 <210> 3166
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 <220>
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 <400> 3166
 agcccggagt aggagtgcgc ctcgttt 27

 <210> 3167
 <211> 27
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 <220>
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 <400> 3167
 agcgcggagt aggagtgcgc ctcgttt 27

<210> 3168
<211> 27
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<220>
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<400> 3168
agcgcggagt aggagtgcgc ctcgttt

27

<210> 3169
<211> 27
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<220>
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<220>
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<223> The residue at this position is a30.

<400> 3169
ccaggaagca agtggtgcgc ctcgttt

27

<210> 3170
<211> 27
<212> DNA
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<220>
<223> Synthetic
<220>

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<222> (3)..(3)

<223> The residue at this position is a30.

<220>

<221> modified_base

<222> (26)..(26)

<223> The residue at this position is u33.

<400> 3170

ccaggaagca agtggtgcgc ctctgtut

27

<210> 3171

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

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<223> The residue at this position is a30.

<220>

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<222> (6)..(6)

<223> The residue at this position is a30.

<220>

<221> modified_base

<222> (26)..(26)

<223> The residue at this position is u33.

<400> 3171
ccaggaagca agtgggtgcgc ctcgtut

27

<210> 3172

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

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<223> The residue at this position is a30.

<220>

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<223> The residue at this position is a30.

<220>

<221> modified_base

<222> (7)..(7)

<223> The residue at this position is a30.

<220>

<221> modified_base

<222> (26)..(26)

<223> The residue at this position is u33.

<400> 3172
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27

<210> 3173

<211> 27

<212> DNA

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<223> The residue at this position is a30.

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<222> (26)..(26)

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27

<210> 3174

<211> 27

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<213> Artificial Sequence

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<223> The residue at this position is a30.

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27

<210> 3175
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13

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<220>
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 <400> 3176
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 ccaggaagca agtggaggcg tgacggt 27

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 ccgtcacgcc tcgccccaca 20

 <210> 3179
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 cttttccata ctttttatga cattc 25

<210> 3180
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14

<210> 3181
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tgtggggcga ggcg

14

<210> 3182
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ccgtcacgcc tcatggataa tgccc

25

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ccgtcacgcc tcagagccaa tcac

24

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31

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gtgattggct ctgaggcg

18

<210> 3190
<211> 18
<212> DNA
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<220>
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<400> 3190
gtgattggct ctgaggcg 18

<210> 3191
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ccgtcacgcc tccaccatat ccc 23

<210> 3192
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<210> 3193
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gggatatggt ggaggcg 17

<210> 3194
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gggatatggt ggaggcg

17

<210> 3195
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18

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<210> 3198
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aacgaggcgc acgcaactcg ca 22

<210> 3199
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aacgaggcgc acgcaactcg ca 22

<210> 3200
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aacgaggcgc acgcaactcg ca

22

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aacgaggcgc acgcaactcg ca

22

<210> 3203

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aacgaggcgc acgcaactcg ca

22

<210> 3204

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ggcctgcaga gactctgc 18

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gccactgcta agcac 15

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aacgaggcgc acctccaatc tca 23

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 aacgaggcgc acctccaatc tca 23

 <210> 3209
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 aacgaggcgc acctccaatc tca 23

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gccaaatctc ctcca

15

<210> 3216
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17

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13

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<220>
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27

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27

<210> 3220
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27

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 aacgaggcgc accaccatat cc 22

 <210> 3222
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 ccggaagaat gggtcgacca tg 22

 <210> 3223
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 ggatatggtg gtgcgc 16

 <210> 3224
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 <400> 3224
 ccggaagaat gggtcgac 18

<210> 3225
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<400> 3225
ccgtcacgcc tcggttgagg ttc

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17